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FIGURE 1

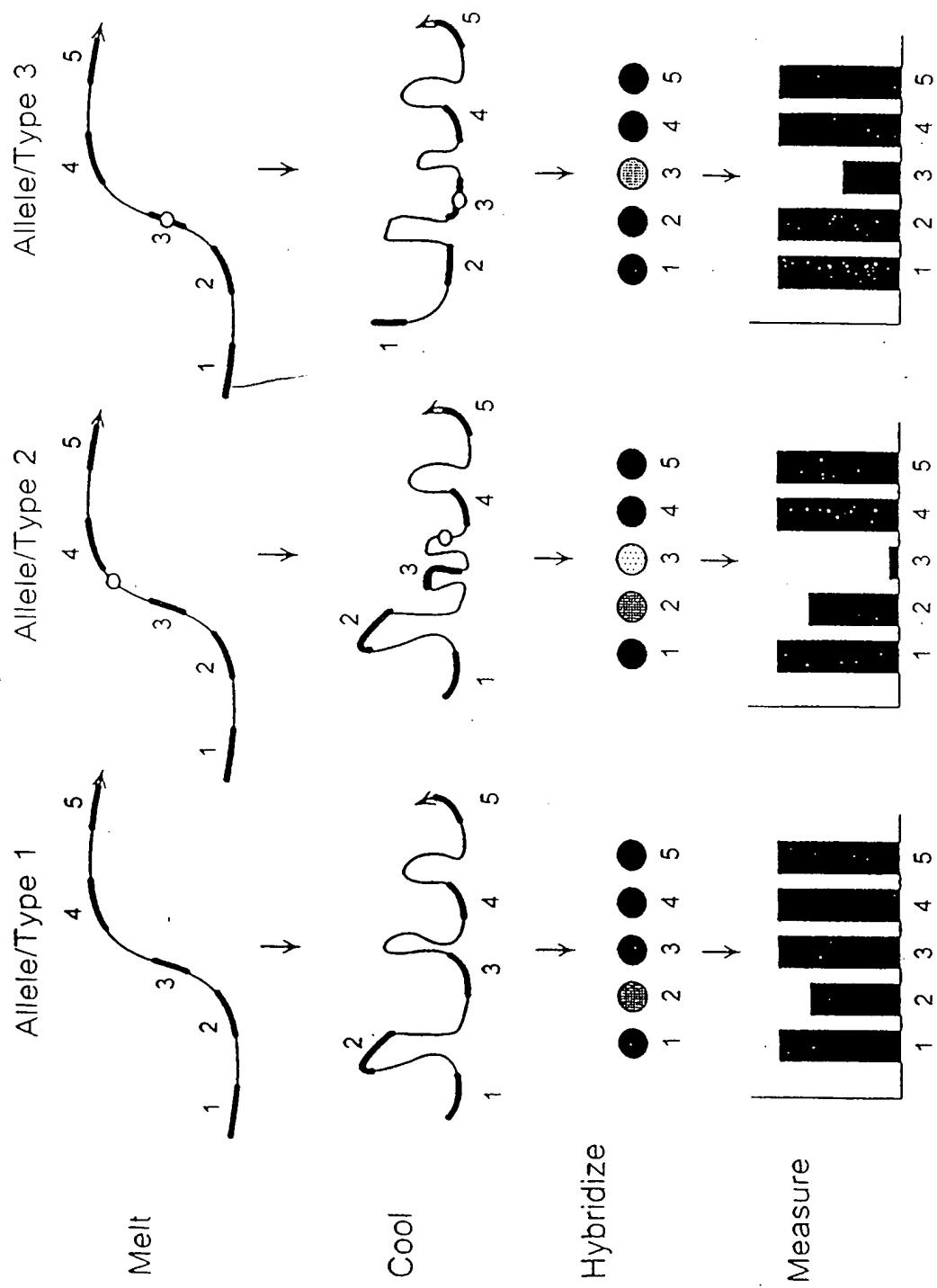


FIGURE 2

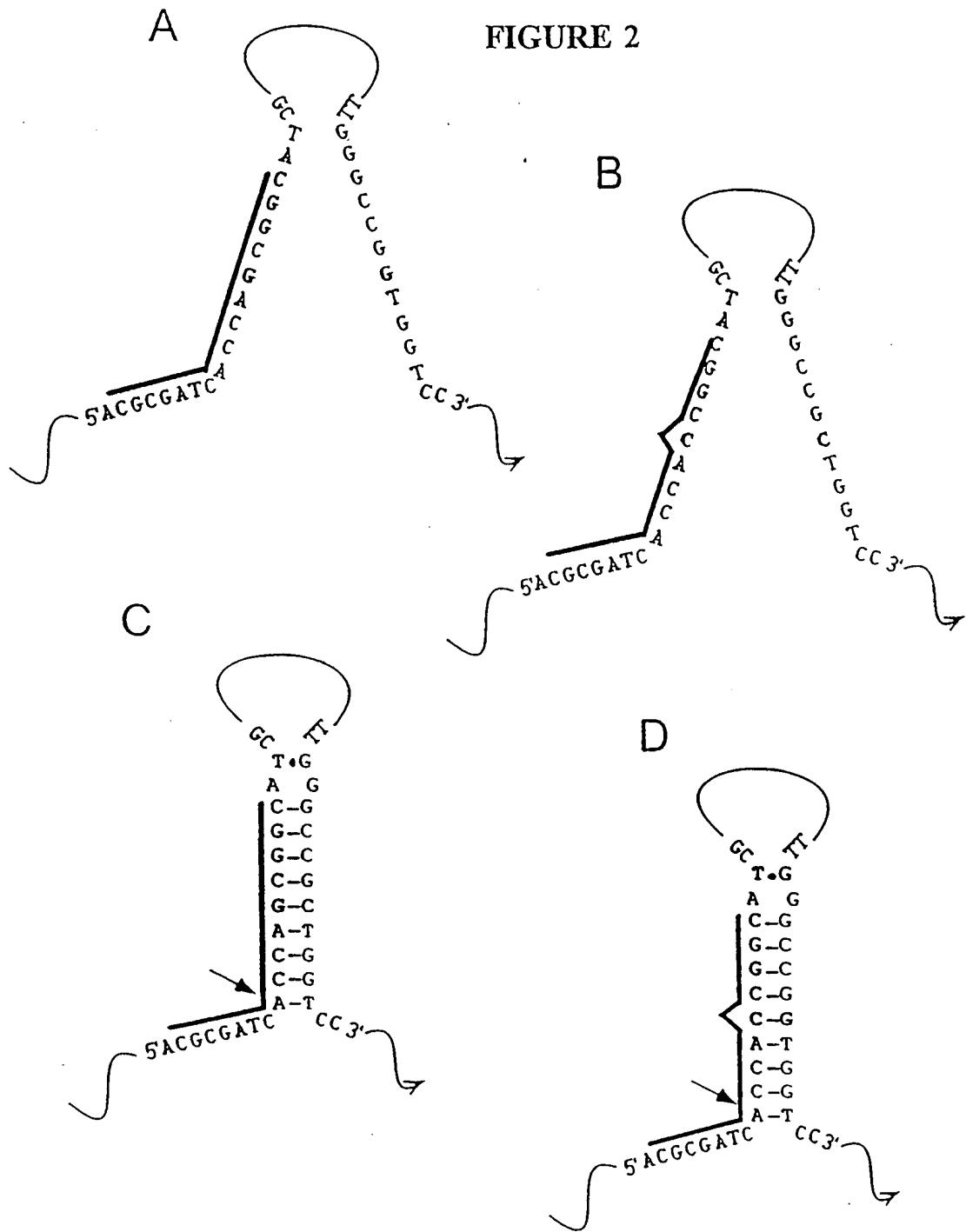


FIGURE 3



FIGURE 4

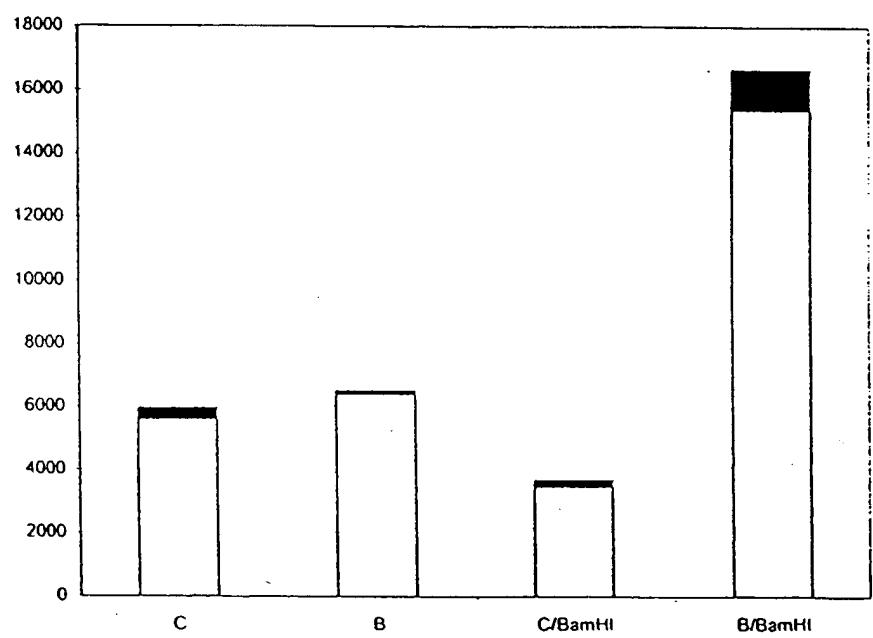


FIGURE 5

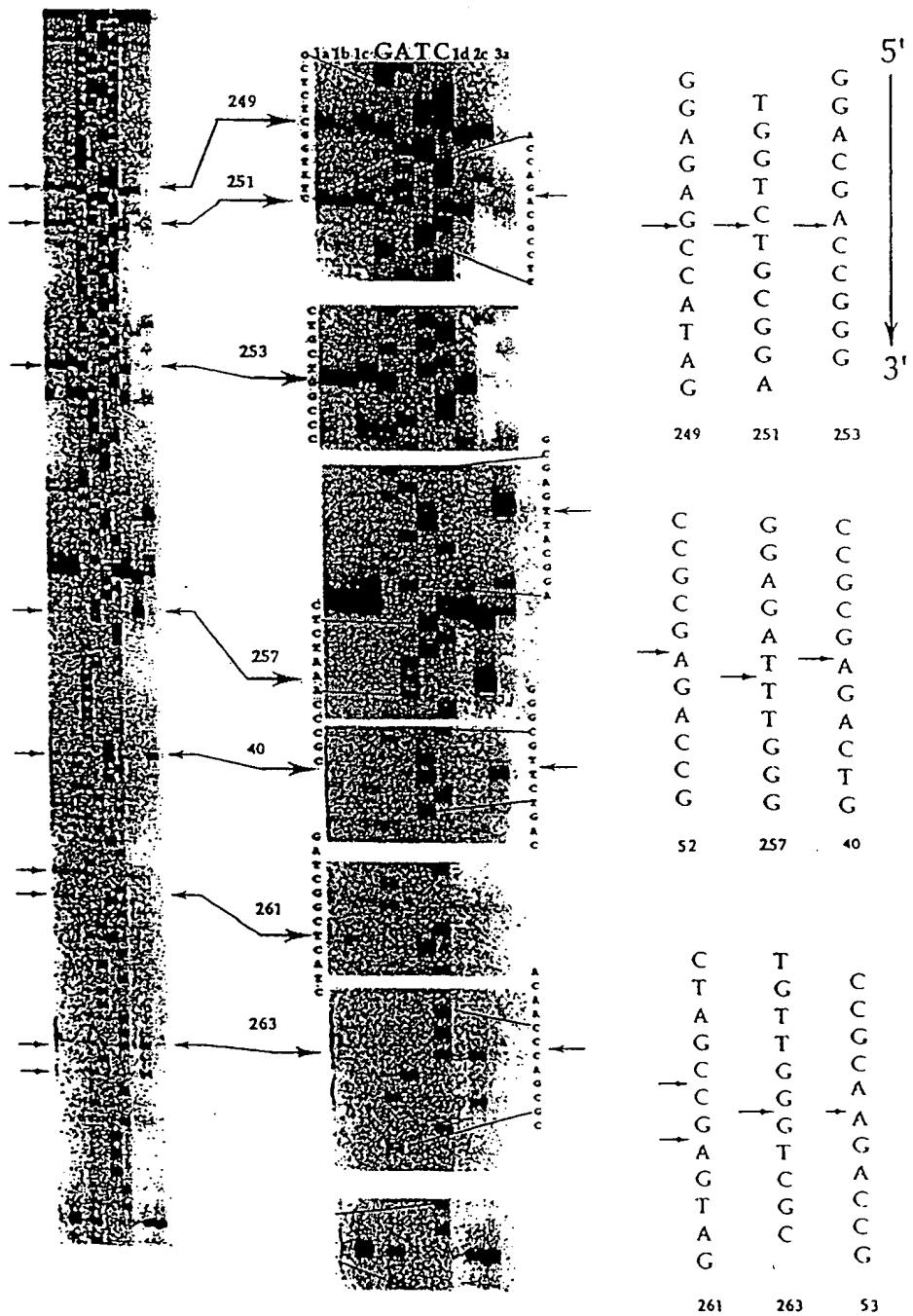


FIGURE 6

Consensus: GATTCCTGCTT TCACGGCAGAA AGCCGTCTAGC CATGGCGTTA GTATGAGTGT CGTGCAGCCCT

HCV 1a -----
HCV 1b -----
HCV 2c -----
HCV 3a -----

#249 CCAGGACCCC CCCCTCCCCGGG AGAGGCCATAG TGGTCTGCGGG AACCCGGTGA G TACACCGGAA

-----T-----
-----C-----
-----A-----

#251 -----

#253 TTGCCAGGAC GACC GG GT CCAACCCGGCTC AATGCCCTGGG AATT TGGGCG

-----G---A---T---
-C---TG---GT-----

#257 -----

-----A---A---T---
-----G-----

#40 #261 #263 TGCCCCCGCA AGACTGCTAG CCGAAGTAGTG TTGGGGTCGCG AAAGGCCTTG TGGTACTGCC

-----G-----
-----C---T---
-----G---TCA-----

TGATAGGGTG CTTGCGAGTG CCCCGGGAGG TCTCGTAGAC CGTGCAATC

-----A-----

FIGURE 7

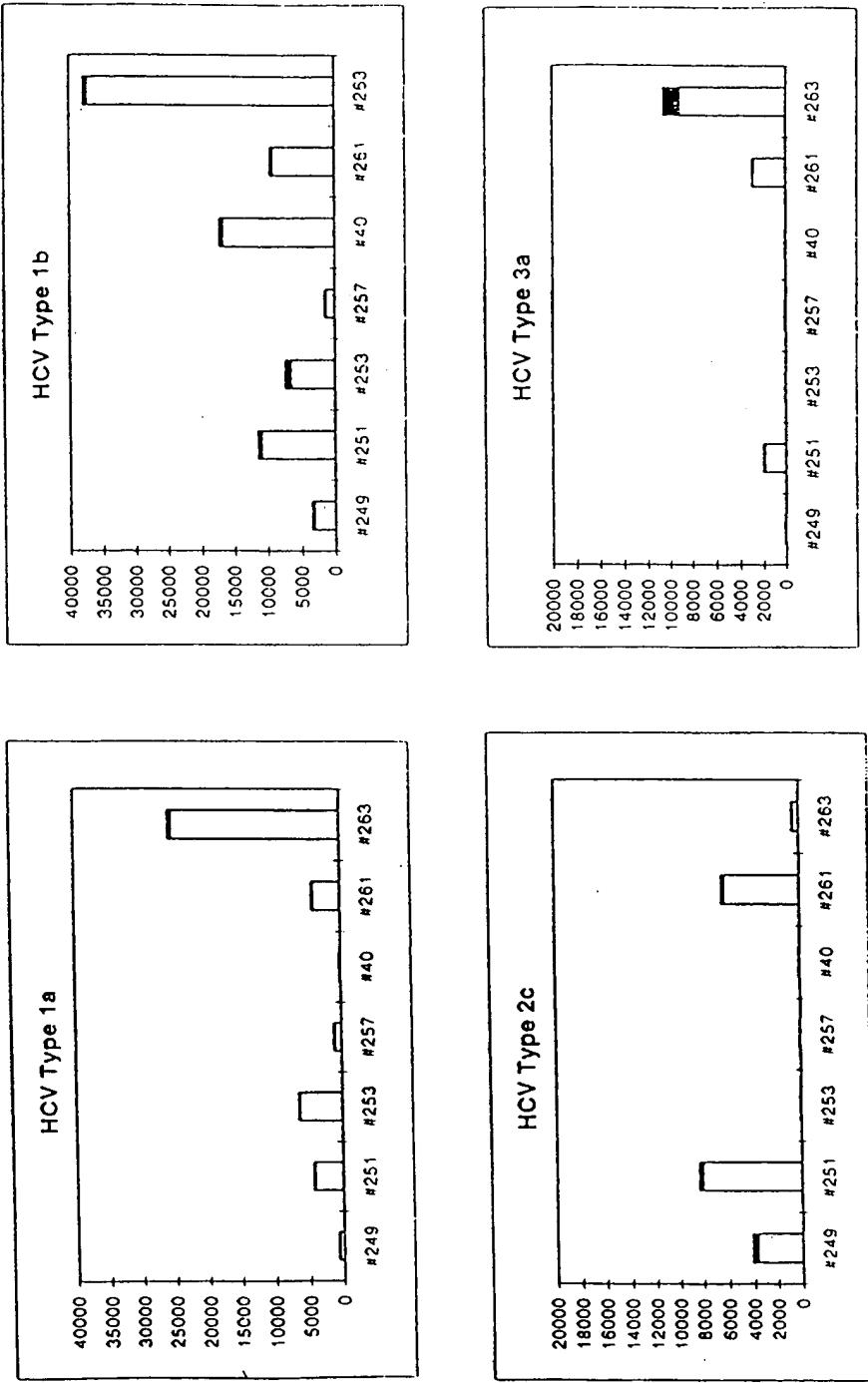


FIGURE 8A

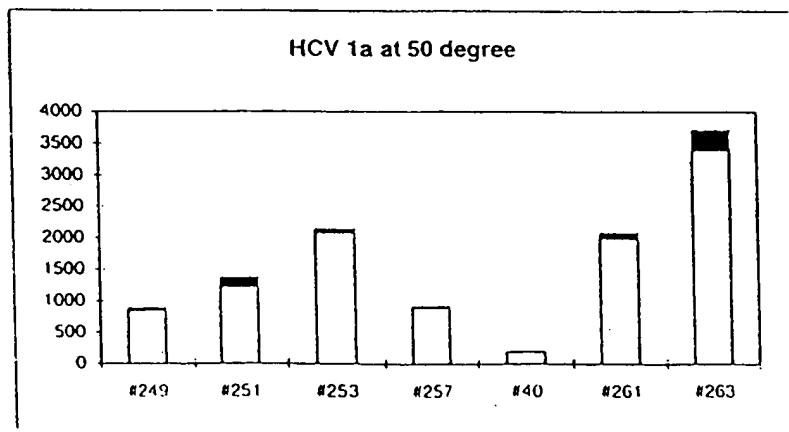
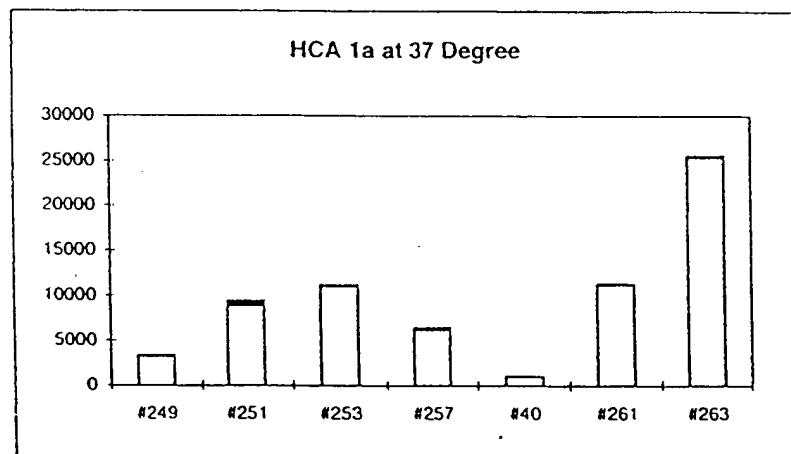
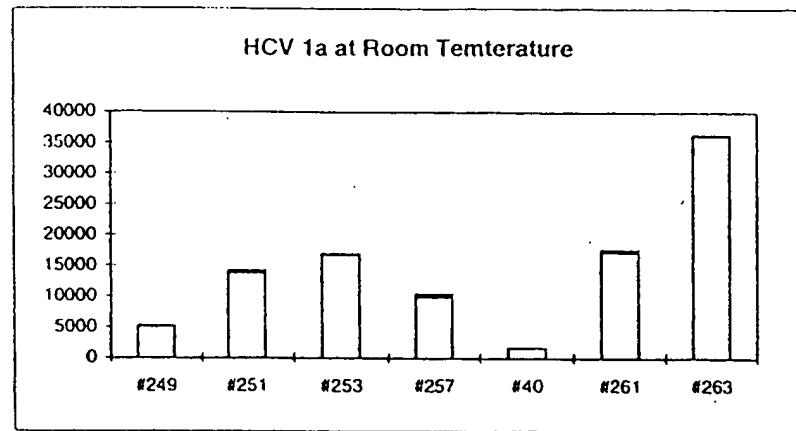


FIGURE 8B

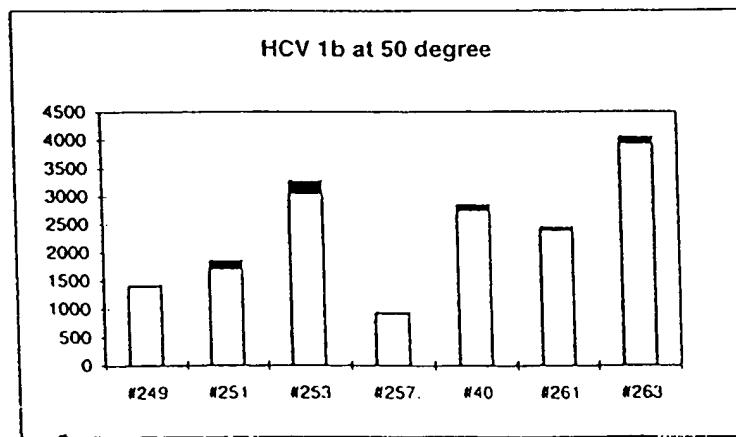
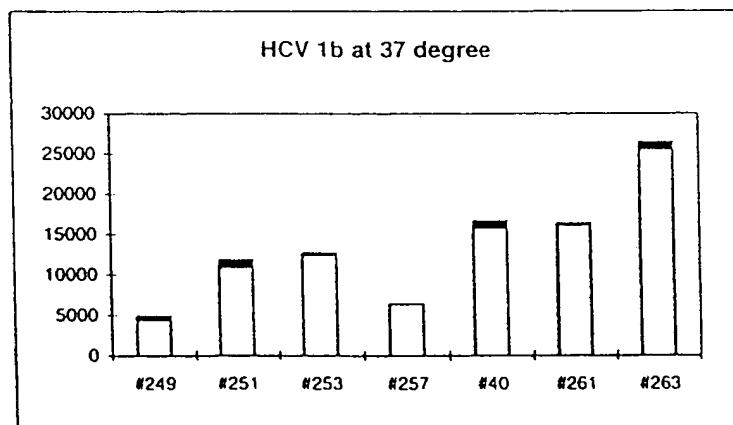
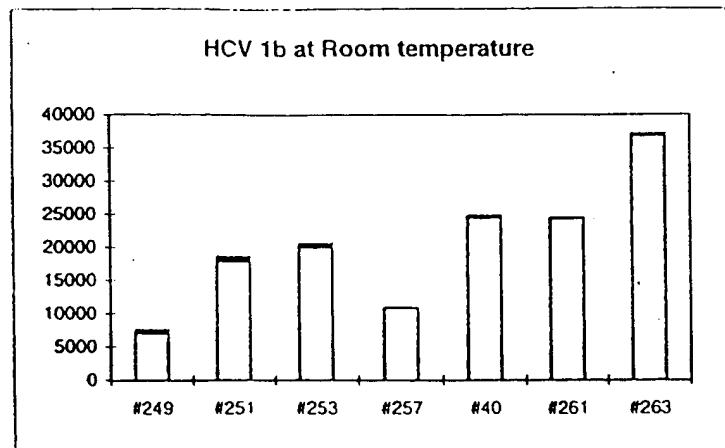


FIGURE 8C

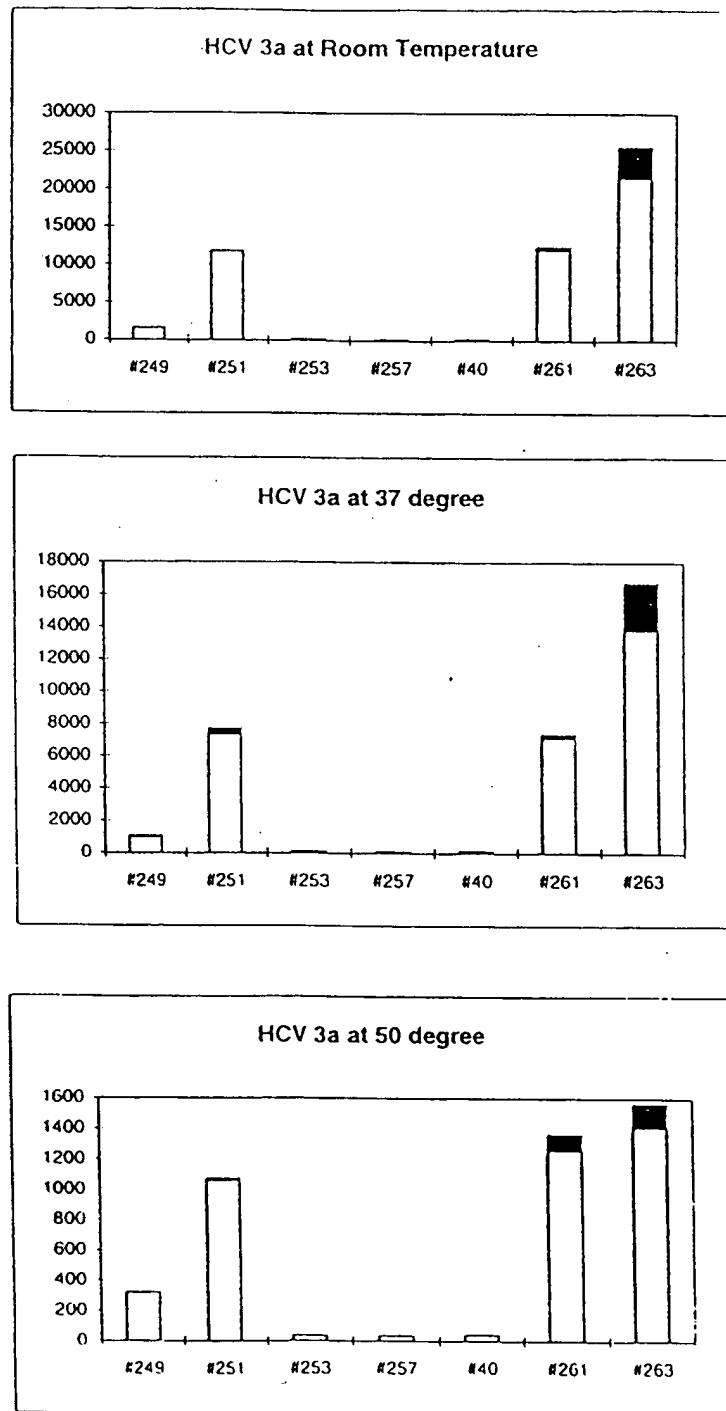


FIGURE 9A

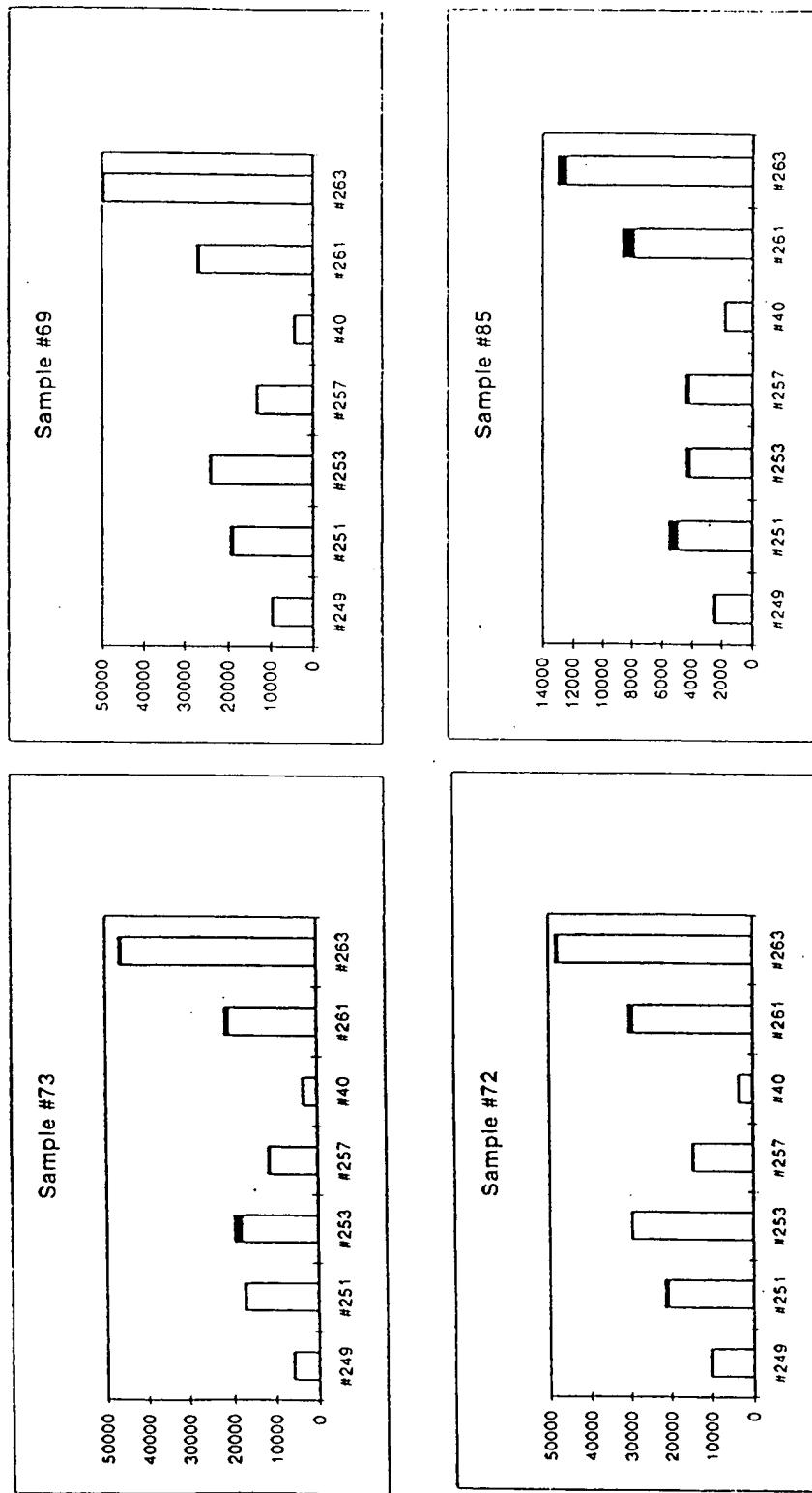


FIGURE 9B

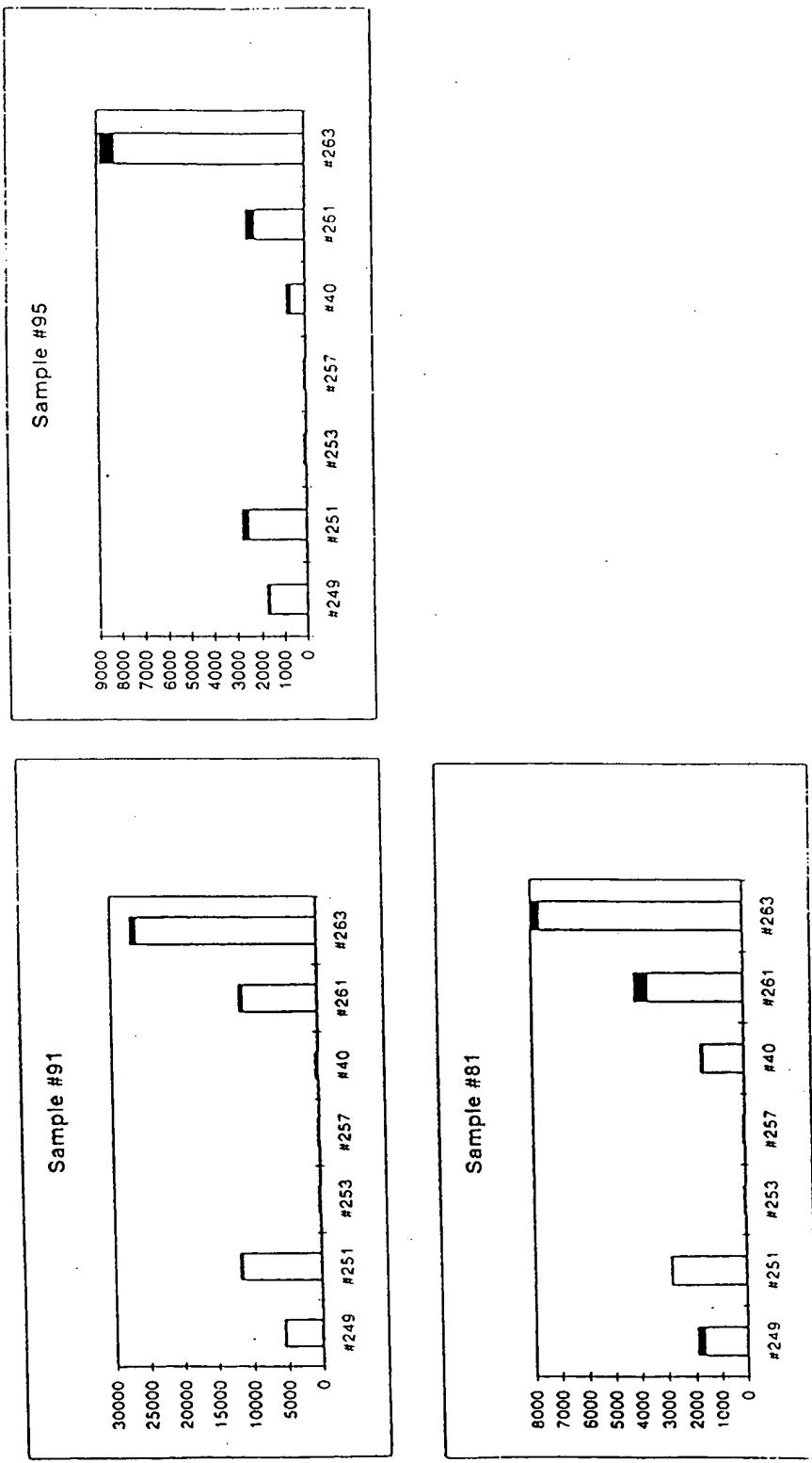


FIGURE 9C

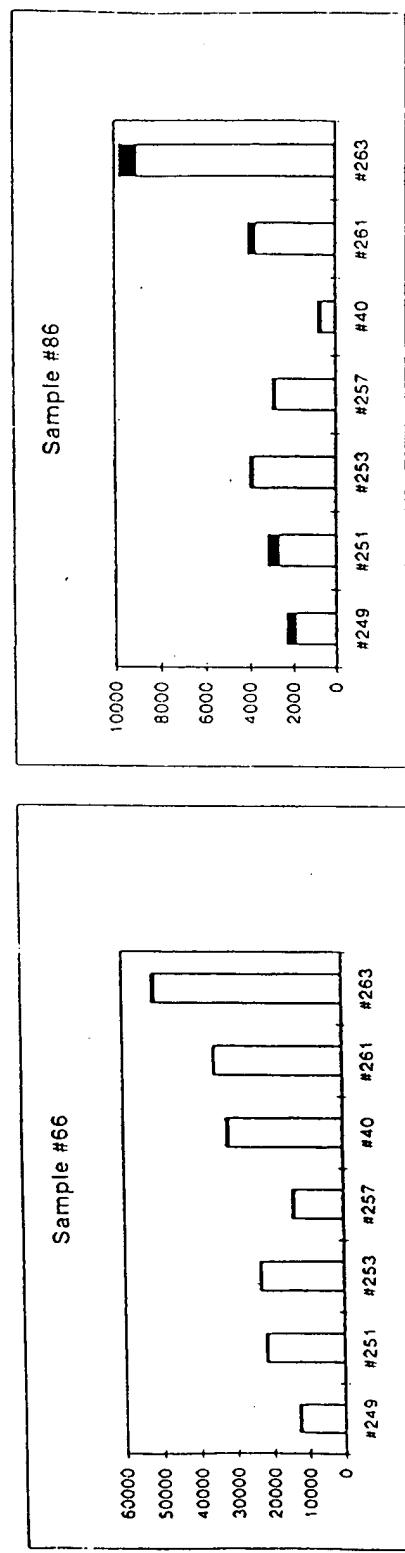


FIGURE 9D

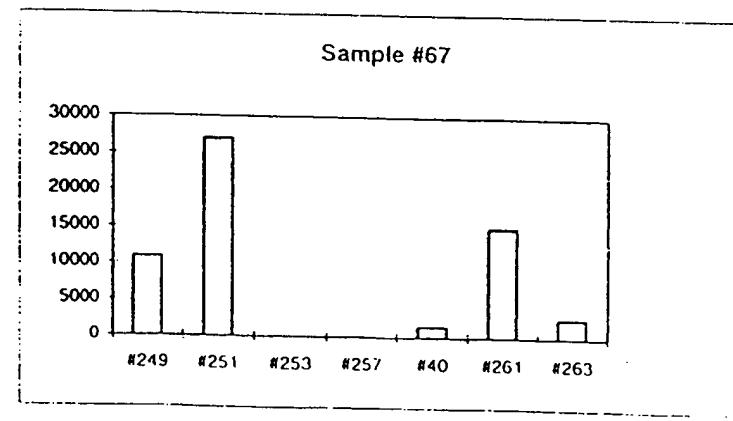
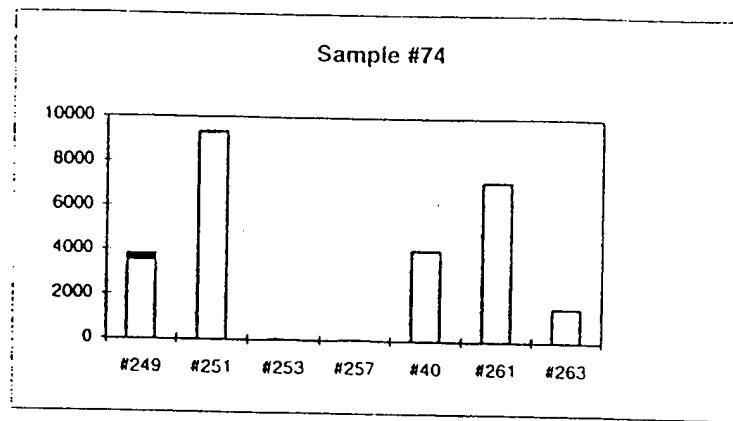


FIGURE 10

A
G A
T — A
C — G
T — A
G — C
T — A
C — G
G — C
C — G
#80
5' - F1-T G C T C T C T G G T T G G T C T C T C G T A A T -3'

A
G A
T — A
C — G
T — A
G — C
T T
C C
G — C
C — G
#81
5' - F1-T G C T C T C T G G T T G G T C T C T C G T A A T -3'

G A A
T T T
C T T
T T T
G T T
C T T
G T T
C T T
#82
5' - F1-T G C T C T C T G G T T G G T C T C T C G T A A T -3'

FIGURE 11A

#2) 5' Biotin

T A
C G A
A T — A
G C — G
A T — A
C G — C
A T — A
G C — G
C G — C
G C — G

#80) 5' - F1-T G C T C T C T G G T T G G T C T C T C G T A A T -3'

#FD91) 3' Biotin - C G A G A G A C C A - 5'

A
G A
T — A
C — G
T — A
G — C
T — A
C — G
G — C
C — G

#80) 5' - F1-T G C T C T C T G G T T G G T C T C T C G T A A T -3'

#78) 3' - A G A C C A T T A C C A G A -Biotin 5'

#4) 3' - G A G A C C A T T A C C A G A G -Biotin 5'

#79) 3' - A G A G A C C A T T A C C A G A G A -Biotin 5'

#116) 3' - A G A G A C C A A C C A G A G A -Biotin 5'
↓ ↓

#117) 3' - T A C C A G A G A -Biotin 5'

#118) 3' - A G A G A C C A T - 5'

FIGURE 11B

A
G A
T — A
C — G
T — A
G — C
T — A
C — G
G — C
C — G
#80) 5' - F1-T G C T C T C T G G T T G G T C T C T C G T A A T -3'
#79) 3' - A G A G A C C A — T T — A C C A G A G A -Biotin 5'

A
G A
T — A
C — G
T — A
G — C
T — A
C — G
G — C
C — G
#80) 5' - F1-T G C T C T C T G G T T G G T C T C T C G T A A T -3'
3' - A G A G A C C A A C C A G A G A -Biotin 5'
#115 T T #114
A A
C C
A ↔ C C ↔ A
A A
G G
C ↔ A A ↔ C
G G
A A
/ /
Biotin 5' 3'

FIGURE 12

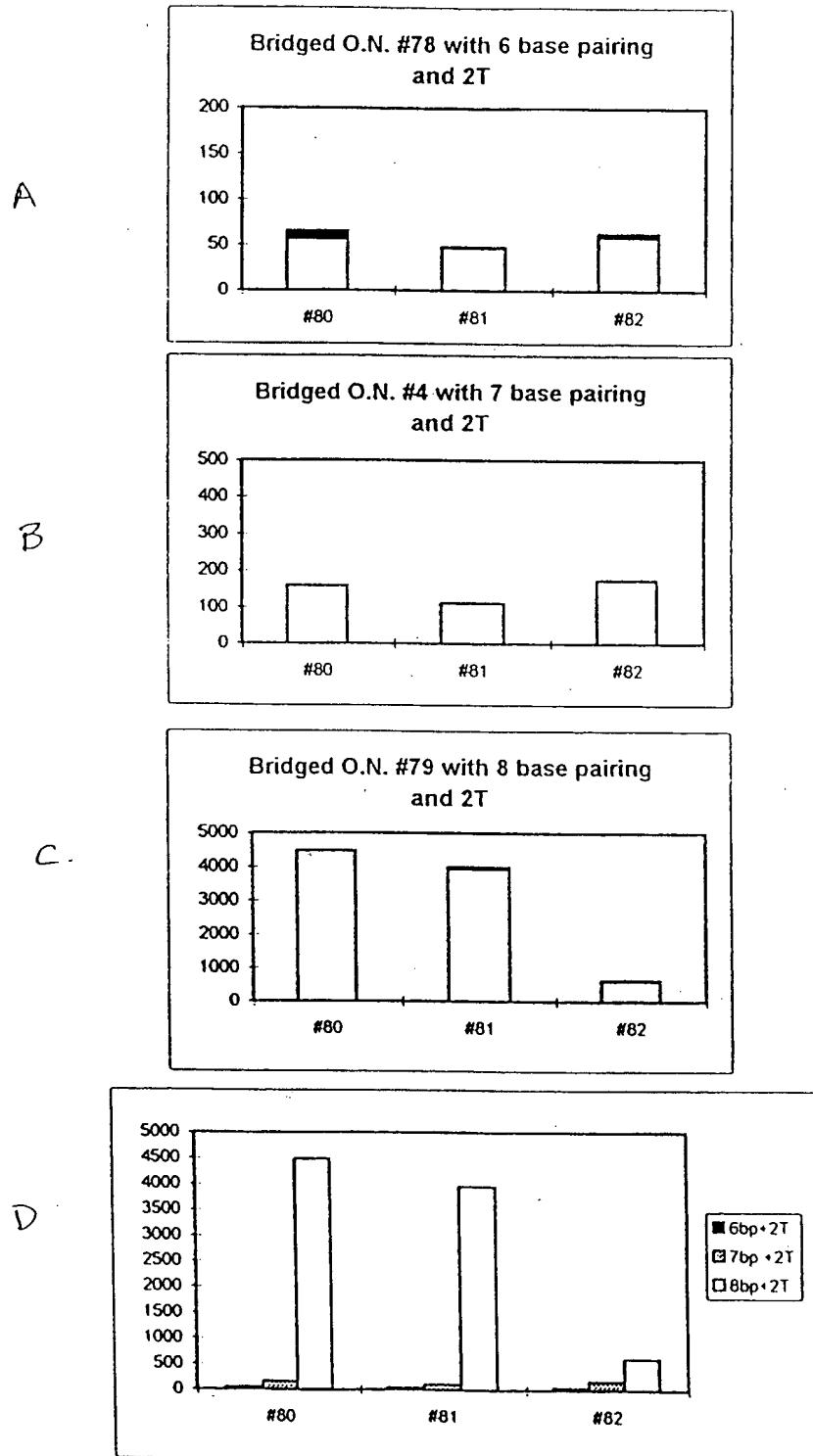


FIGURE 13A

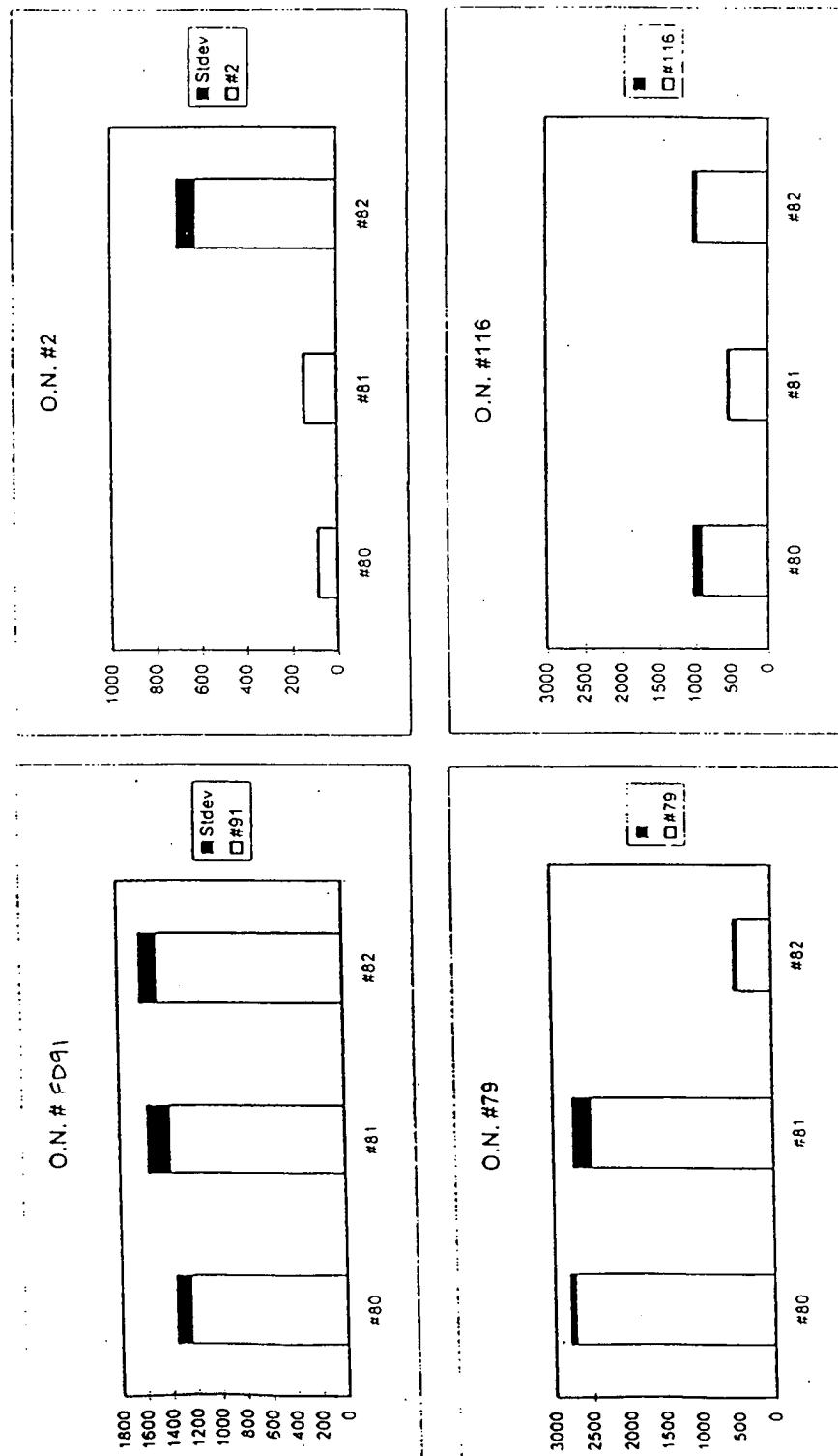


FIGURE 13B

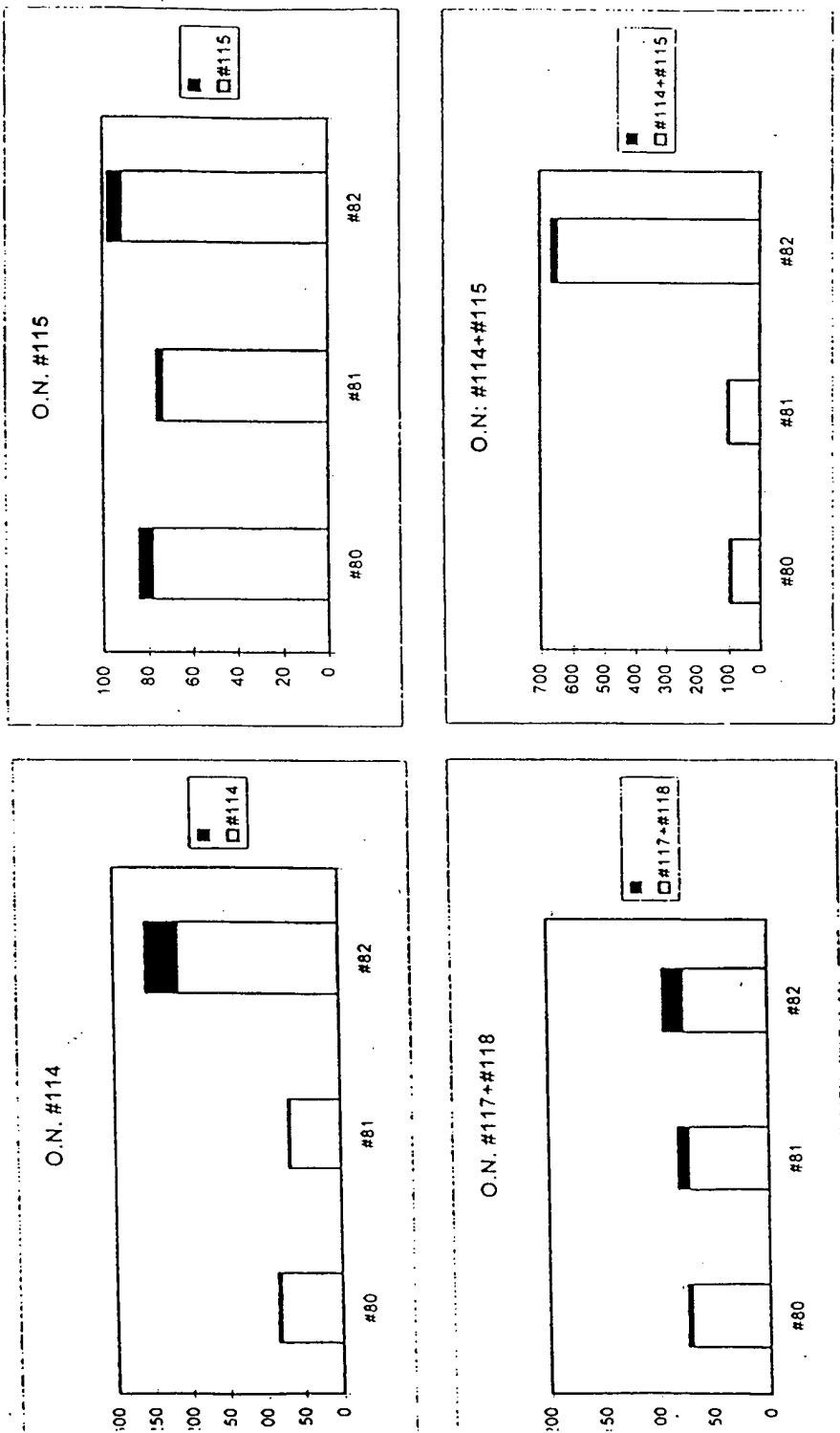


FIGURE 14

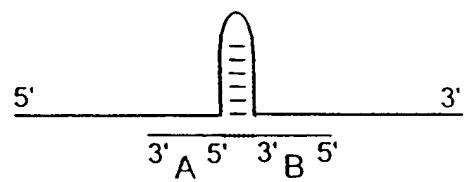
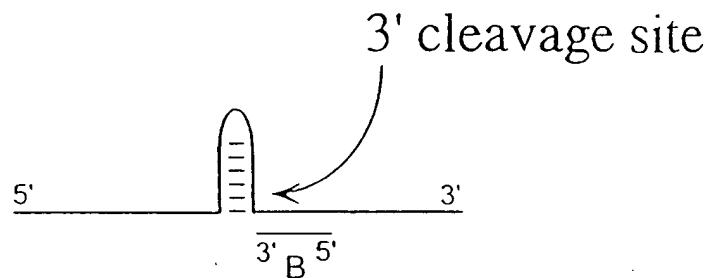
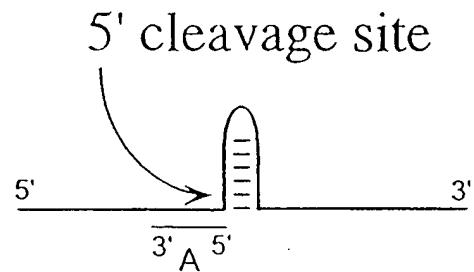


FIGURE 15

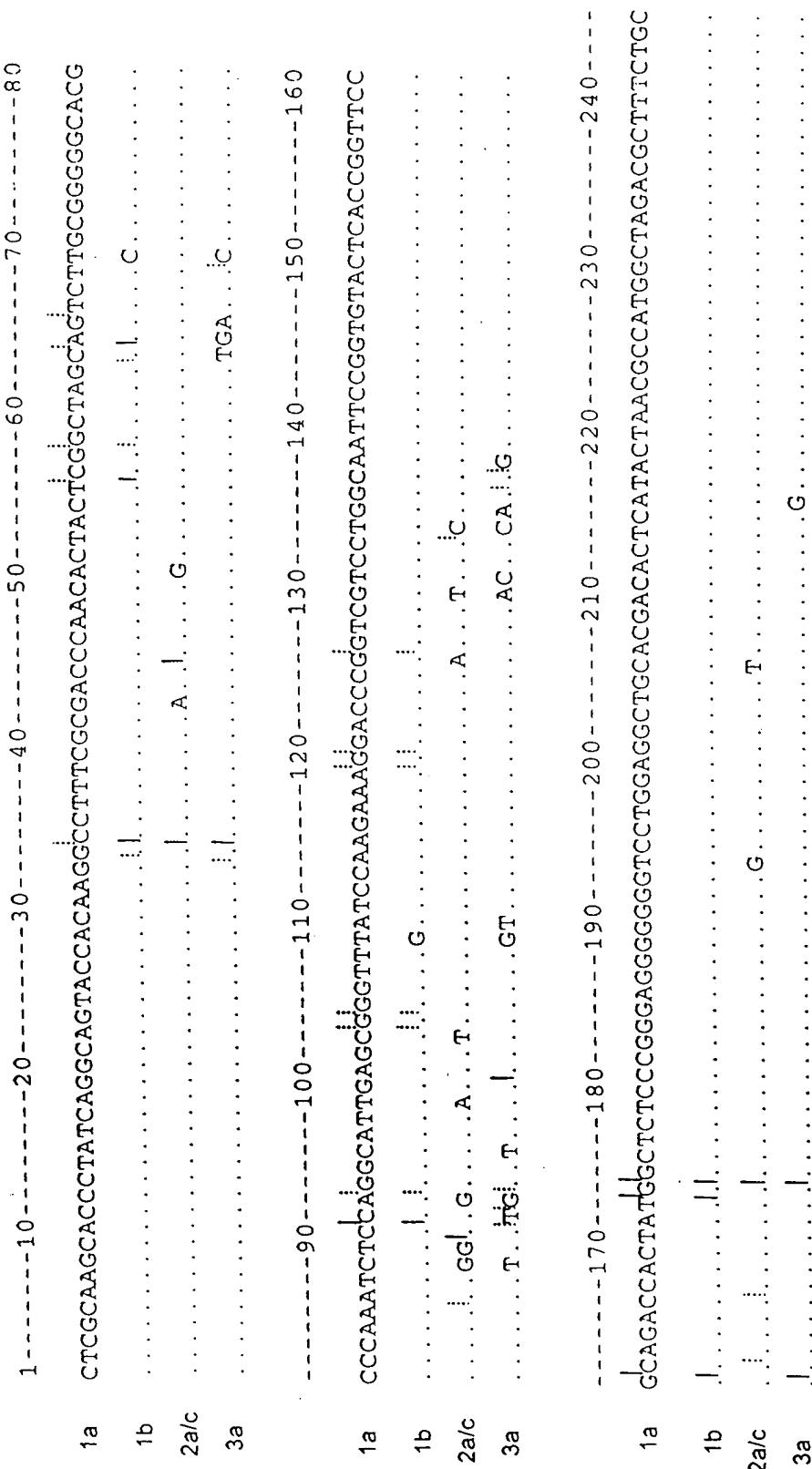


FIGURE 16A

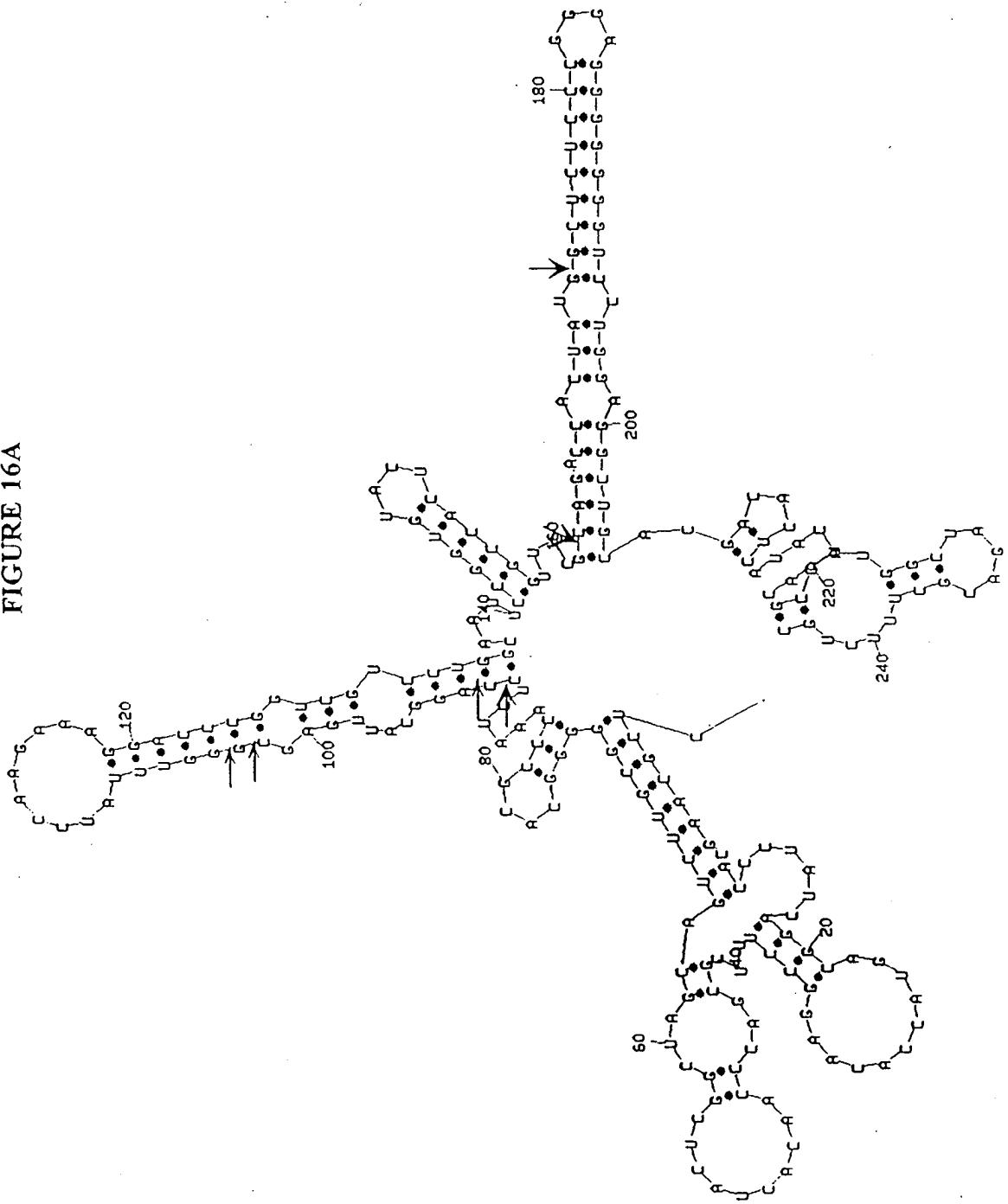


FIGURE 16B

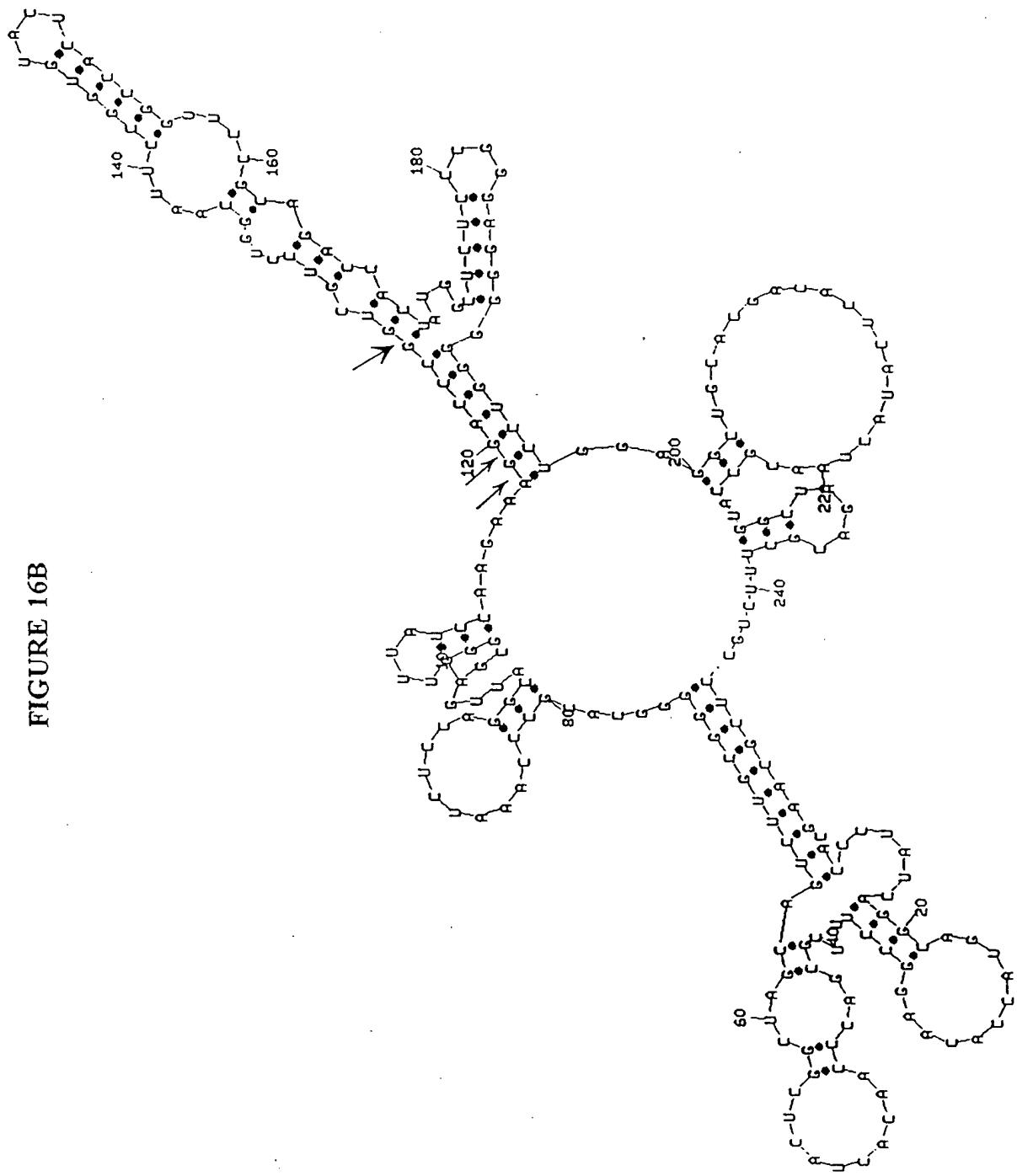


FIGURE 17A

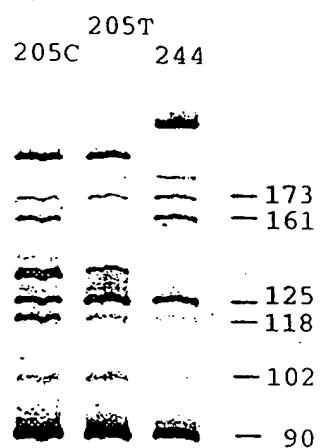


FIGURE 17B

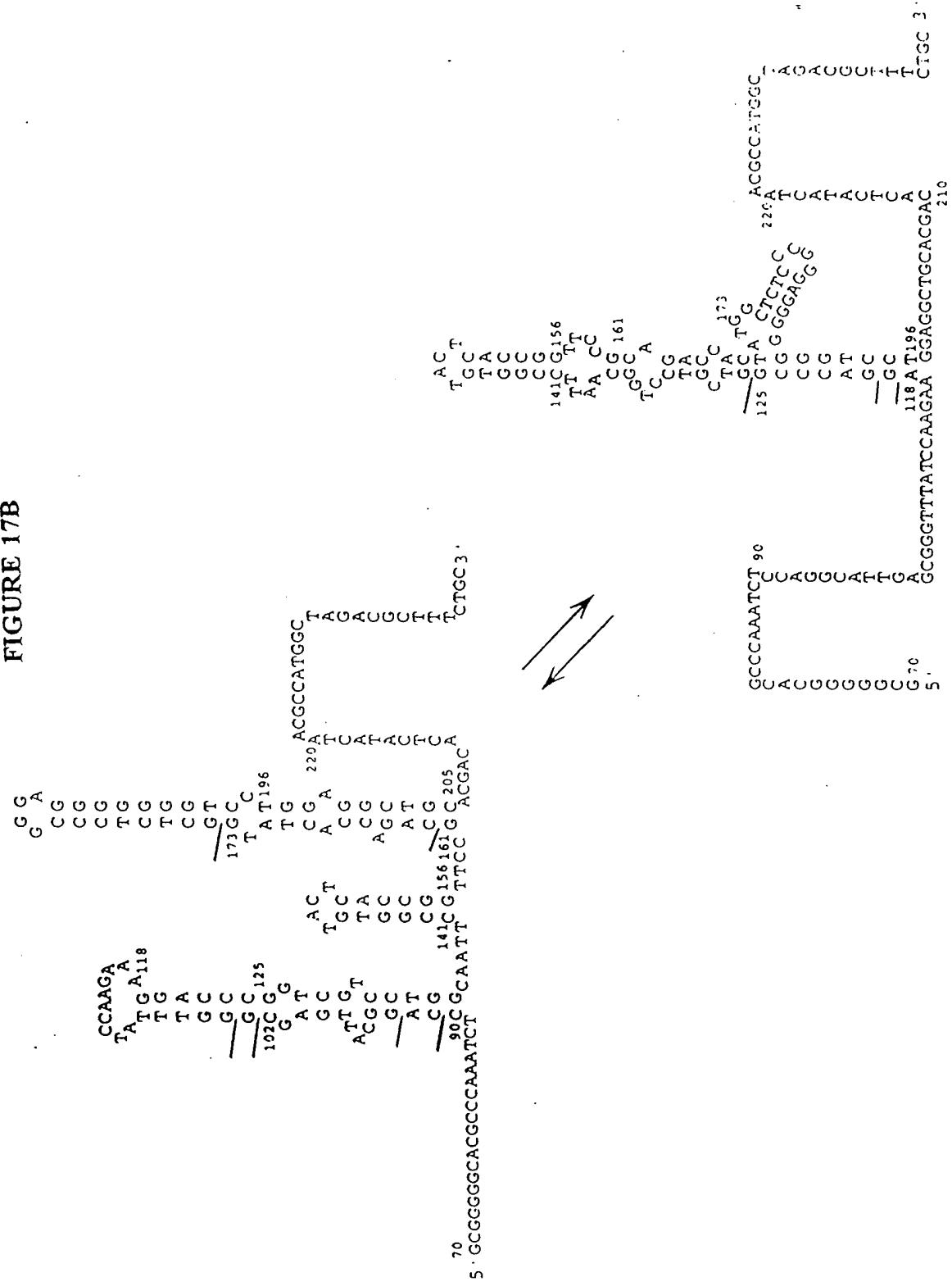


FIGURE 17C

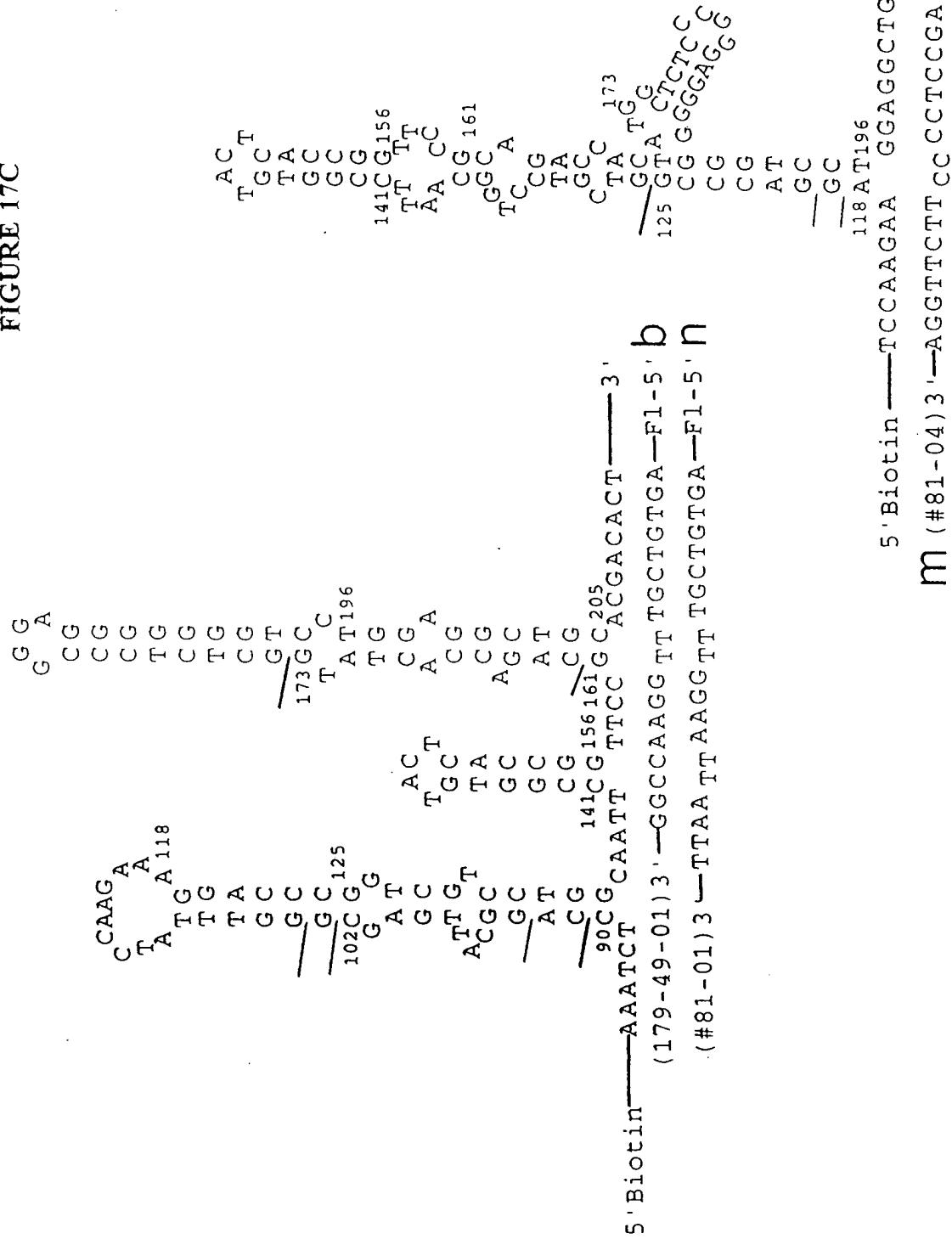


FIGURE 18A

HCV 1a

TCV 1a

	G G
C AAG	G A
T A	C G
A 118	C G
T G	T G
T G	C G
T A	T G
G C	C G
G C	G T
G C	173 G C
102 C G 125	T C
G G	A T 196
A T	T G
G C	C G
A T G T	A A
C G C	C G
G C	A G C
A T	A T
C G	C G
70 90 C G 141 C G 156 161 G C 205	ACGACACT — 3 ·
— TGCGGGGCACGCCAAATCT CAATT TTCC —	b
(179-49-01) 3 · GGCCAAGG <u>TT</u> TGCTGTGA 5 ·	b
(192-72-01) 3 · GGCCAAGG <u>AA</u> TGCTGTGA 5 ·	i
(192-72-02) 3 · GGCCAAGG <u>AC</u> TGCTGTGA 5 ·	j
(192-72-03) 3 · GGCCAAGG — TGCTGTGA 5 ·	k
(192-72-04) 3 · GGCCTAGG <u>TT</u> TGCTGTGA 5 ·	C
(192-72-05) 3 · GGCCAAGG <u>TT</u> TGCAGTGA 5 ·	d

FIGURE 18B

HCV 1b

		G G	
		G A	
		C G	
		C G	
	T CCAAGA	C G	
	A A	T G	
	G T G G ^{A118}	C G	
	T A	T G	
A G C	G C	C G	
T A	G C	G T	
CG	G C		
CT	G C	173 G C	
GC	102 C G ¹²⁵	T C	
AT	G G	A T ¹⁹⁶	
GC ⁷⁰	A T	T G	
CG	G C	C G	
GC	T A C	A A	
CG	T G G C	C G	
TG	T G C	C G	
TG	G C	A G C	
TG	G C	C G	
CG C A	A T	A T	
CG C	C G	C G	
GC	90 C G ¹⁴¹	156 G C ¹⁶¹	
GC	CAAATCT	TTCC	ACGACACT—3'
(179-49-01) 3' GGCCAAGG <u>TT</u> TGCTGTGA 5' b			
(192-72-01) 3' GGCCAAGG <u>AA</u> TGCTGTGA 5' i			
(192-72-02) 3' GGCCAAGG <u>AC</u> TGCTGTGA 5' j			
(192-72-03) 3' GGCCAAGG — TGCTGTGA 5' k			
(192-72-04) 3' GGCCTAGG <u>TT</u> TGCTGTGA 5' c			
(192-72-05) 3' GGCCAAGG <u>TT</u> TGCAGTGA 5' d			

FIGURE 18C

HCV 2a/c

C	AAG	
C	A	
C	A ¹¹⁸	
A	T A	
A	T G	
	T G	G G A
	T A	G G
	G C	C G
	G C	C G
	G C	C G
	102 T A ¹²⁵	T G
	G A T G	C G
	G C	T G
	A T	C G
	T A T	G C
	C A T	173 G C ¹⁹⁶
	G C	T A T
	G C	T G
	G C	C G
	C G T A C	A A
	90 C G G C	C G
	G C T A	C G
	G A G C	A G C
	T A G C	A T
	A T C G	C G
	5' — CACGCCCAA T C G ¹⁴¹ 156 161 G ²⁰⁵ — 3'	T GCTGTGA
	(179-49-01) 3' GGCCAAGG _{TT} TGCTGTGA 5' b	
	(192-72-01) 3' GGCCAAGG _{AA} TGCTGTGA 5' i	
	(192-72-02) 3' GGCCAAGG _{AC} TGCTGTGA 5' j	
	(192-72-03) 3' GGCCAAGG — TGCTGTGA 5' k	
	(192-72-04) 3' GGCCTAGG _{TT} TGCTGTGA 5' C	
	(192-72-05) 3' GGCCAAGG _{TT} TGCAGTGA 5' d	

FIGURE 18D

HCV 3a

CAAG
C A

T A	G A	
T A 118	G G	
G G	G C G	
T G	C G	
T A	C G	
G C	C G	
G C	T G	
G C	C G	
102 C G 125	T G	
G G	C T	
A T	G C	
G C	173 G C	
A T T A C	T A T 196	
T G C	T G	
G C	C G	
G C T T	A A	
T A G C	C G	
90 C G T A	C G	
T G C G C	A G C	
T A G C	A T	
A T C G	C G	
A T C G 156 161	G C 205	
CACGCCCA	TTCC	ACGACACT

5' — CACGCCCA — TTCC — ACGACACT — 3'

(179-49-01) 3' GGCCAAGG TT TGCTGTGA 5' b

(192-72-01) 3' GGCCAAGG AA TGCTGTGA 5' i

(192-72-02) 3' GGCCAAGG AC TGCTGTGA 5' j

(192-72-03) 3' GGCCAAGG — TGCTGTGA 5' k

(192-72-04) 3' GGCCTAGG TT TGCTGTGA 5' C

(192-72-05) 3' GGCCAAGG TT TGCA GTGA 5' d

FIGURE 19

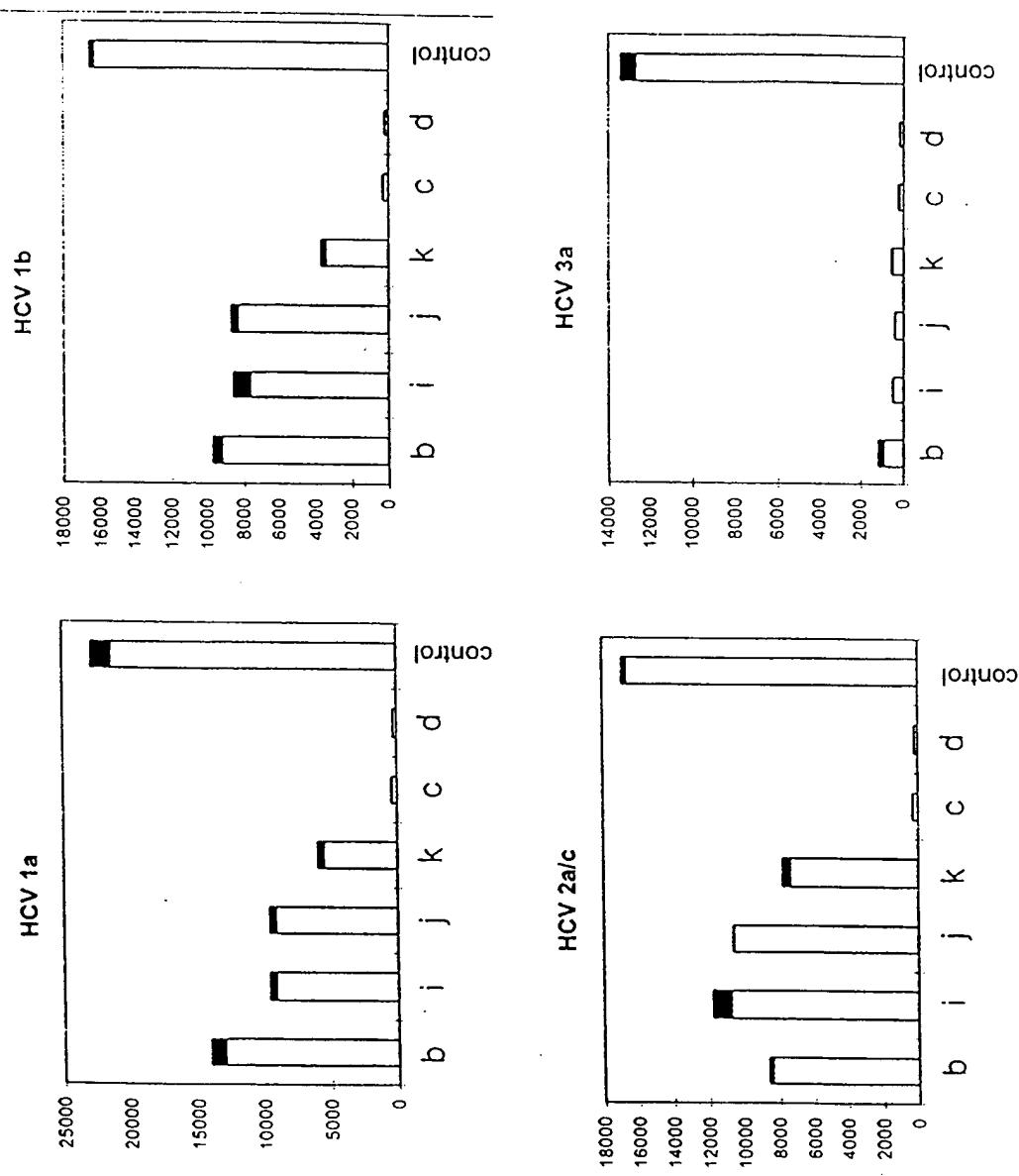


FIGURE 20A

G G
G A

CG

CG

CG

CG

TG

CG

TG

CG

GT

GT

173

GC

C

T A T 196

TG

CG

A A

CG

CG

AGC

CG

AT

CG

CG

ACG

ACT

CG

CG

ACG

ACG

ACG

ACG

ACG

ACG

ACG

ACG

ACG

HCV 1a

5' - C A A T T C C G G T T A C T C A C C G G T T C C G C²⁰⁵ A C G A C A C T — 3'

3' - G G C C A A G G G T T T G C T G T G A - F1' 5' (205-13-02) a

3' - G G C C A A G G G T T T G C T G T G A - F1' 5' (179-49-01) b

3' - G G C C T A G G T T T G C T G T G A - F1' 5' (192-72-04) c

3' - G G C C A A G G G T T T G C A G T G A - F1' 5' (192-72-05) d

3' - G G C C A A G G G - F1' 5' (205-27-01) e

FIGURE 20B

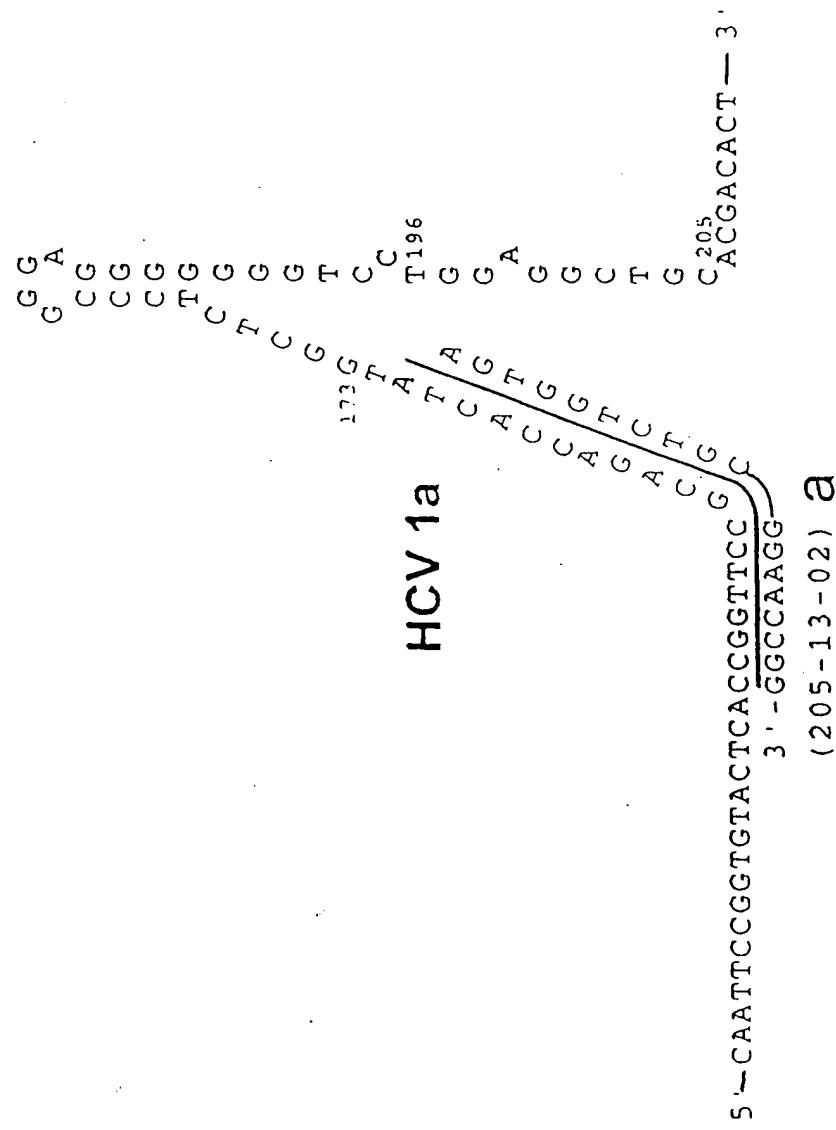


FIGURE 21

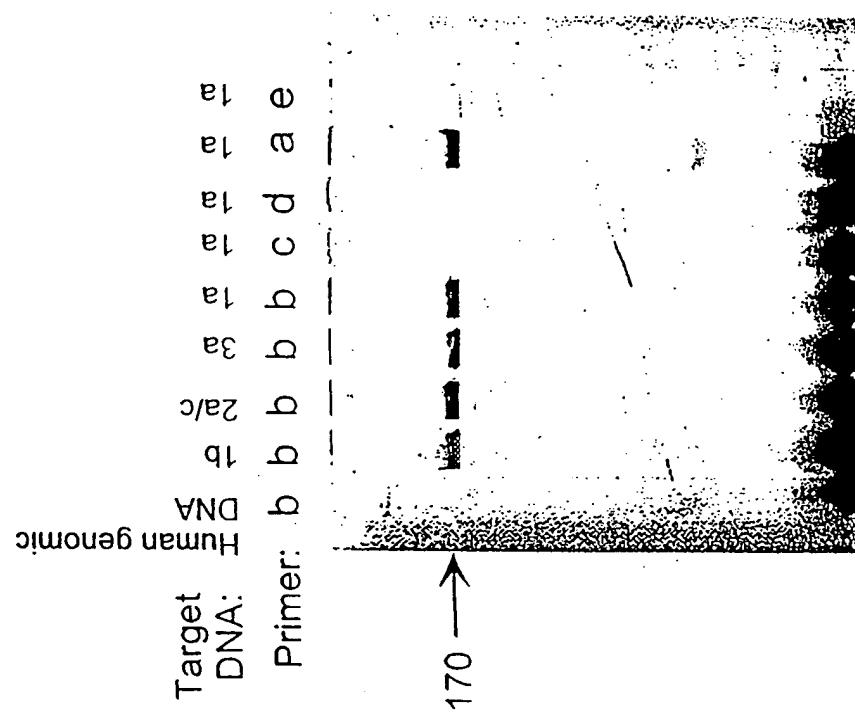


FIGURE 22

G G
G A
C C
C C
C C
T G
C G
T G
C G
G T

173 G C
T A T 196
C G
A G C
A A
C G
C G
A T
C G

HCV 1a

5' - CAATCCGGTACTCACCGTTCC G C²⁰⁵ ACGACACT — 3'

3' - GGCCAAGGCCGTCTGGTGA-F1' 5' (205-13-02) a

3' - GGCCAAGGTTTGCTGGTGA--F1' 5' (179-49-01) b

3' - GGCCAAGG-F15' (205-27-01) e

FIGURE 23

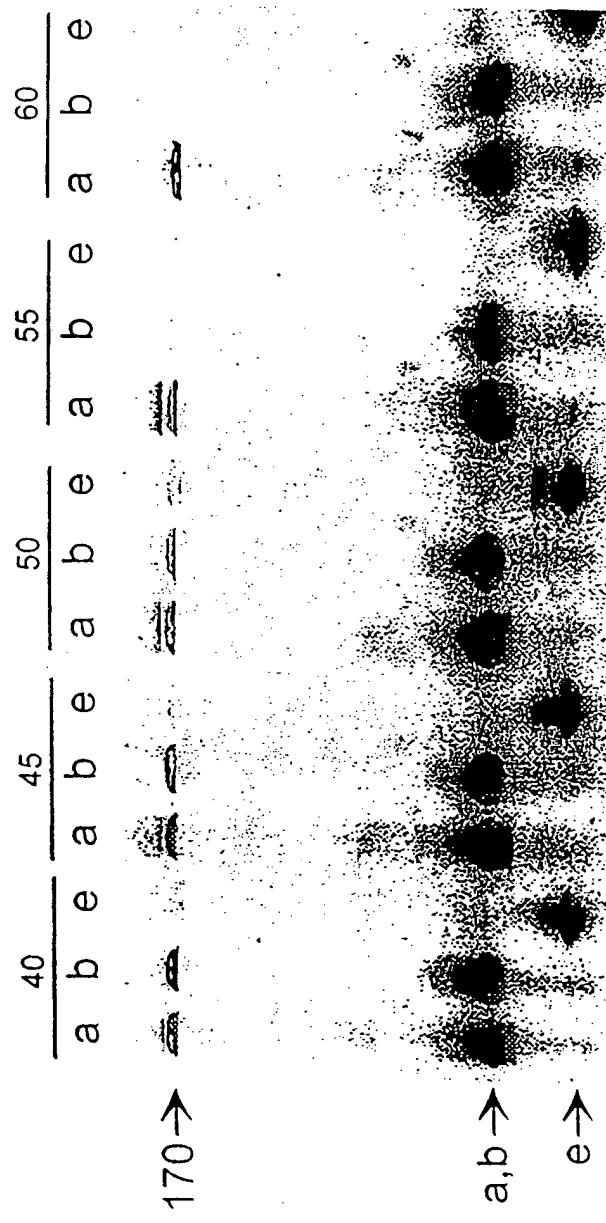


FIGURE 24

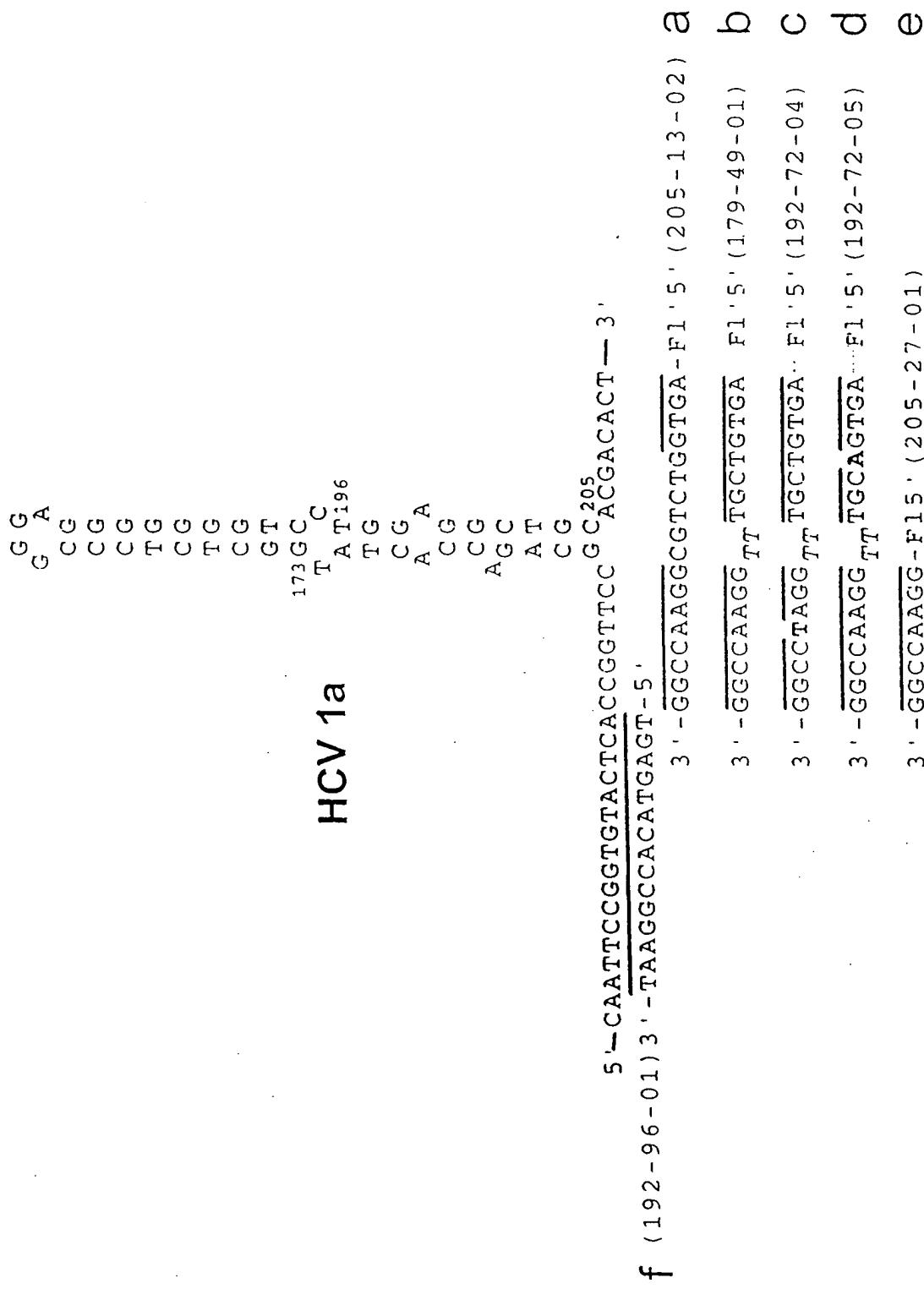


FIGURE 25

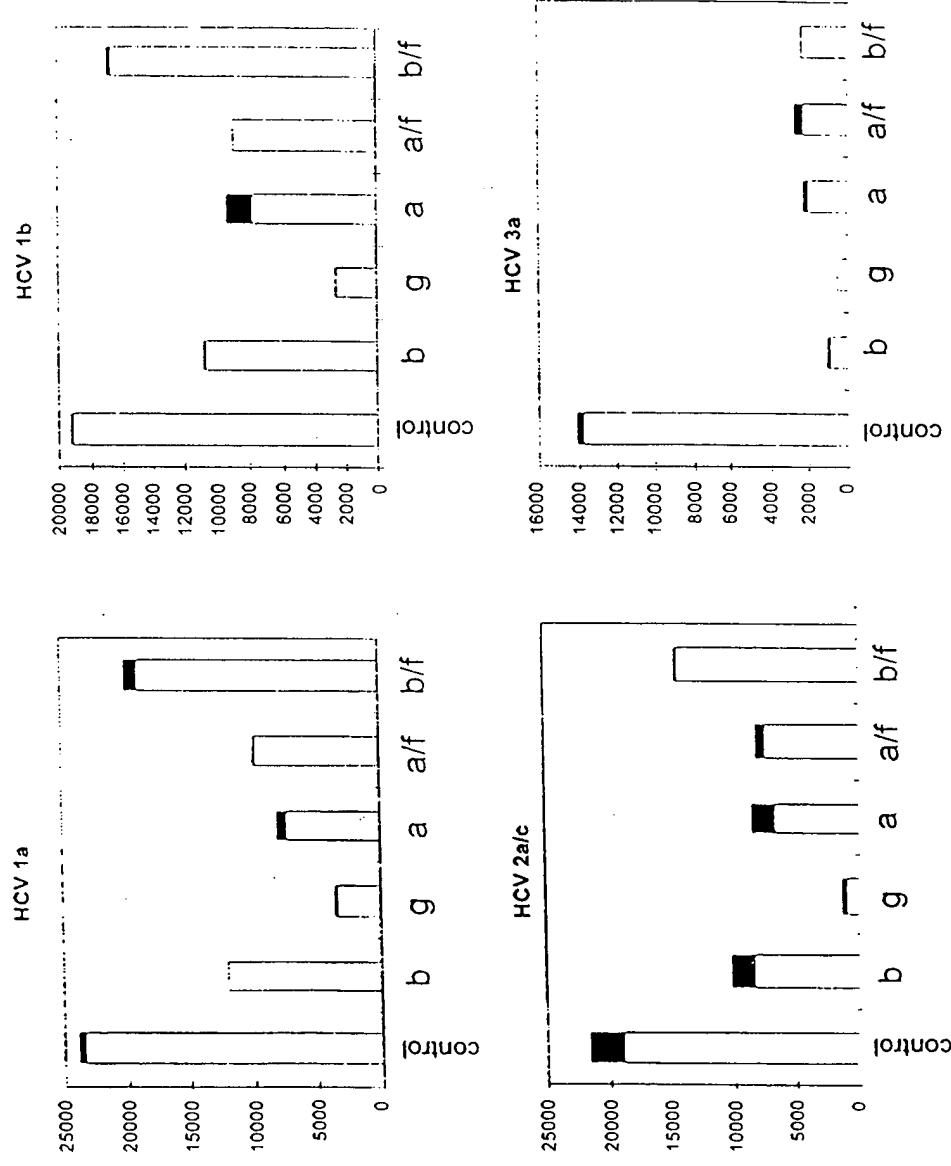


FIGURE 26

5' - ATTCCGGTACTCACCGGTTCCAACGACACT-3' (205-13-01) S.T.
f (192-96-01) 3' - TAAGGCCACATGAGT-5'
3' - GCCCAAGGCCGTCTGGTGA-F1' 5' (205-13-02) a
3' - GCCCAAGG TT TGCTGTGA---F1' 5' (179-49-01) b
3' - GCCCTAGG TT TGCTGTGA---F1' 5' (192-72-04) c
3' - GCCCAAGG TT TGCAAGTGA F1' 5' (192-72-05) d
3' - GCCCAAGG -F15' (205-27-01) e

FIGURE 27

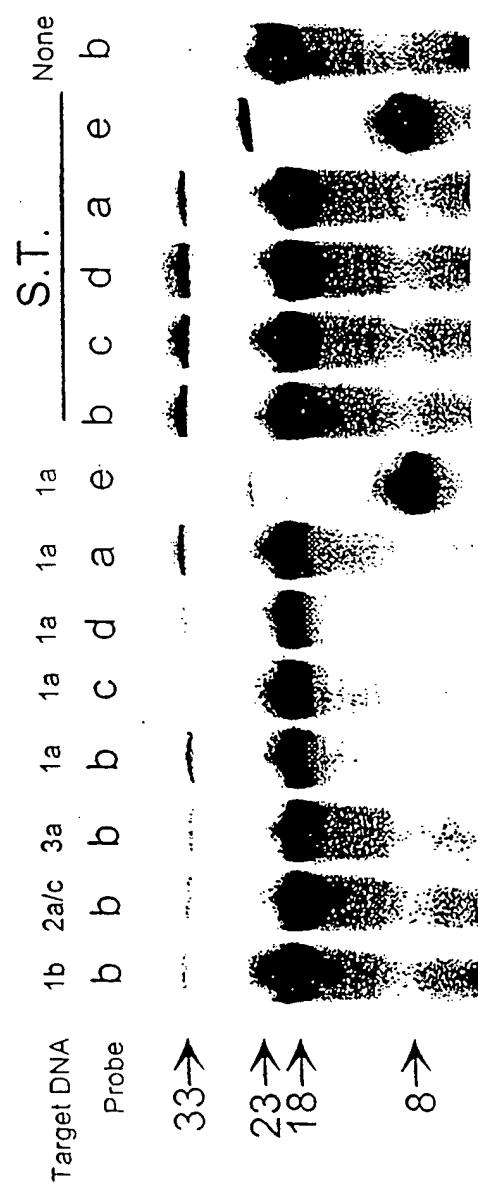


FIGURE 28

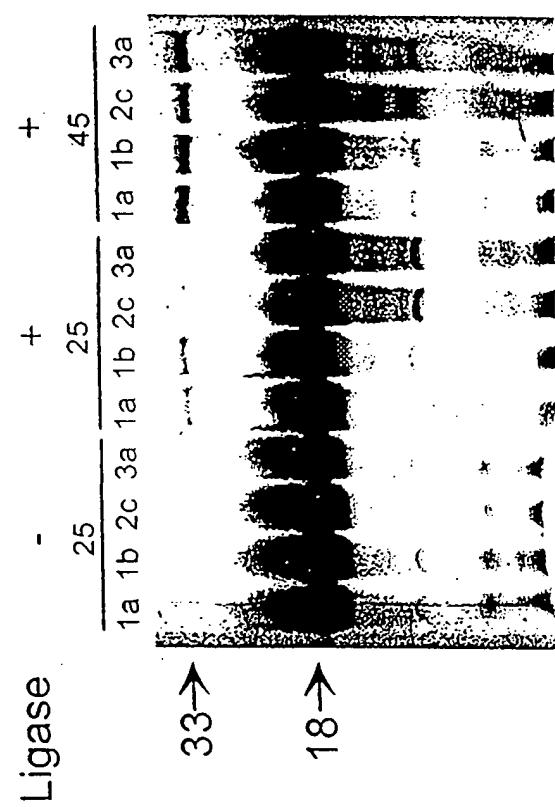


FIGURE 29A

G G
G A
C G
C G
C G
T G
C G
T G
C G
G T
173 G C
T C
A T 196

HCV 1a

T G
C G
A A
C G
C G
A G C
A T
C G

5' - CAATTCCGGTACTCACCGTTCC GC²⁰⁵ ACAGACACT - 3'
3' - GGCCAAGG TT TGCTGTGA - F1' 5' (205-13-02) a
b 3' - GGCCAAGG TT TGCTGTGA - F1' 5' (179-49-01)
c 3' - GGCCTAGG TT TGCTGTGA - F1' 5' (192-72-04)
d 3' - GGCCAAGG TT TGCAGTGA F1' 5' (192-72-05)
e 3' - GGGCCACATGAGTG TT F1' 5' (205-27-01)
f 3' - TAGGCCACATGAGTG TT F1' 5' (192-96-02)

FIGURE 29B

5' - ATTCCGGTGTACTCACCGGTTCCAAACGACACT- 3' (205-13-01) S.T.
3' - GGCCAAGGCCGTCTGGTGA-F1'5' (205-13-02) a
3' - GGCCAAGG TT TGCTGTGA--F1'5' (179-49-01) b
3' - GGCCTAGG TT TGCTGTGA--F1'5' (192-72-04) c
3' - GGCCAAGG TT TGCAAGTGA--F1'5' (192-72-05) d
3' - GGCCAAGG TT TGCAAGTGA--F1'5' (192-72-05) e
9 3' - TAAGGCCACATGAGTGT T T--F1'5' (192-96-02)

FIGURE 30

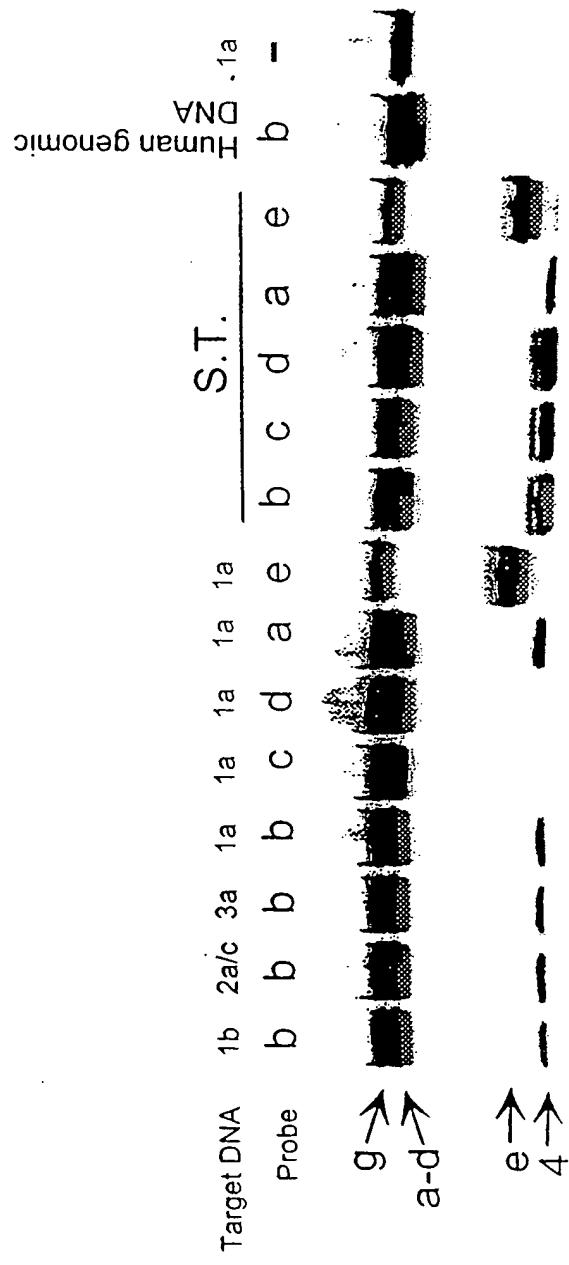


FIGURE 31

G G A
G G C G C G C G T G C G C G G T
173 G C C
T A T 196
T G C G A A C G C G C G A G C A T C G
HCV 1a

5'—CAATTCCGGTGTACTCACCGGTTCC GC²⁰⁵ ACCGACACT—3'
3'—GGCCAAGG TT TGCTGTGA...F1' 5' (179-49-01) b
h (10 bp) 3'—CACATGAGTG TT TT—F1' 5' (205-81-01)

FIGURE 32

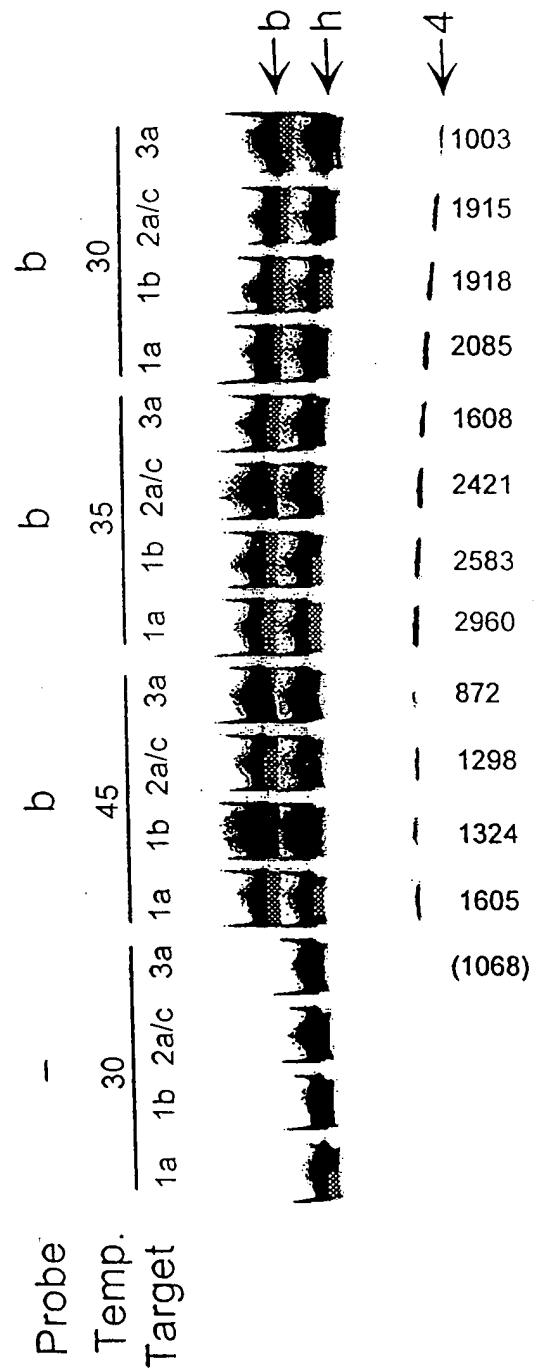


FIGURE 33

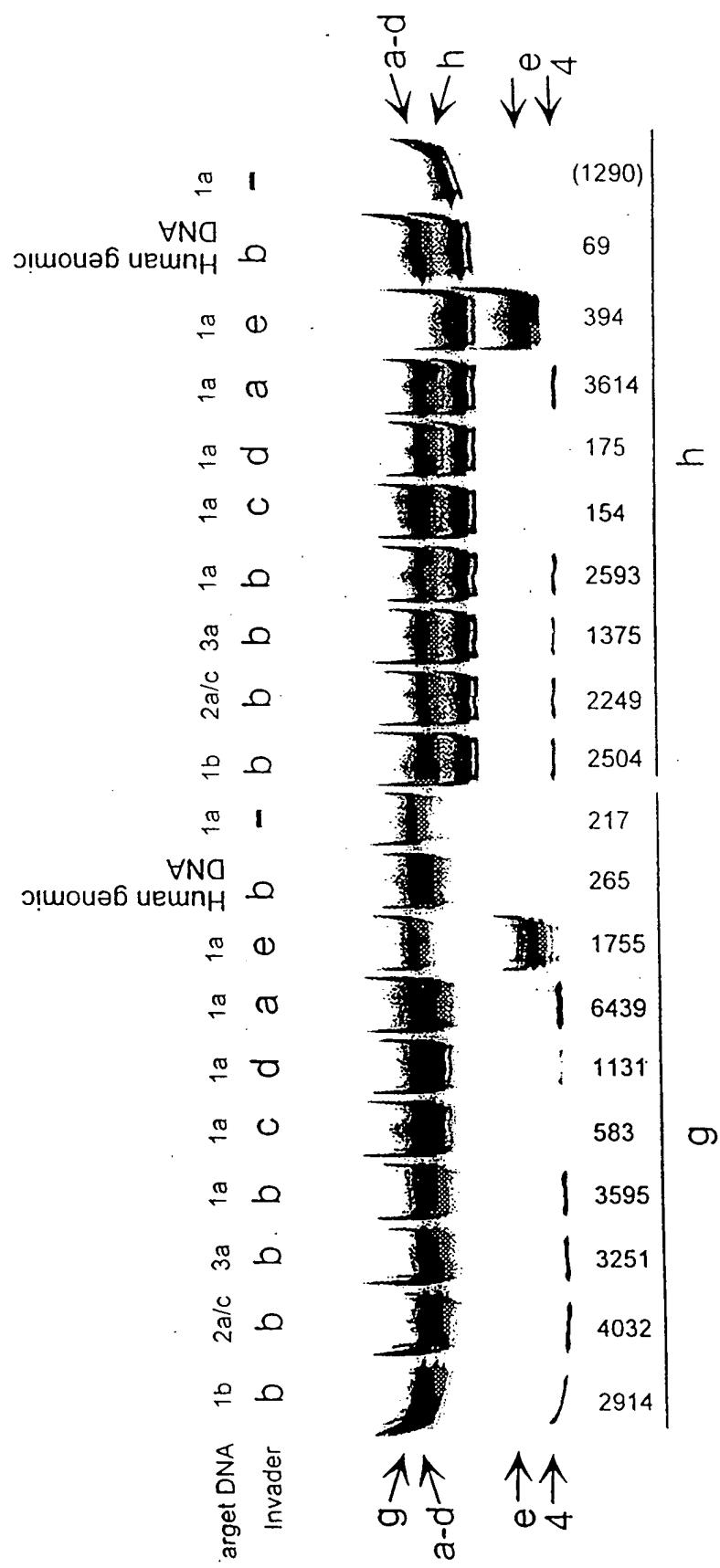
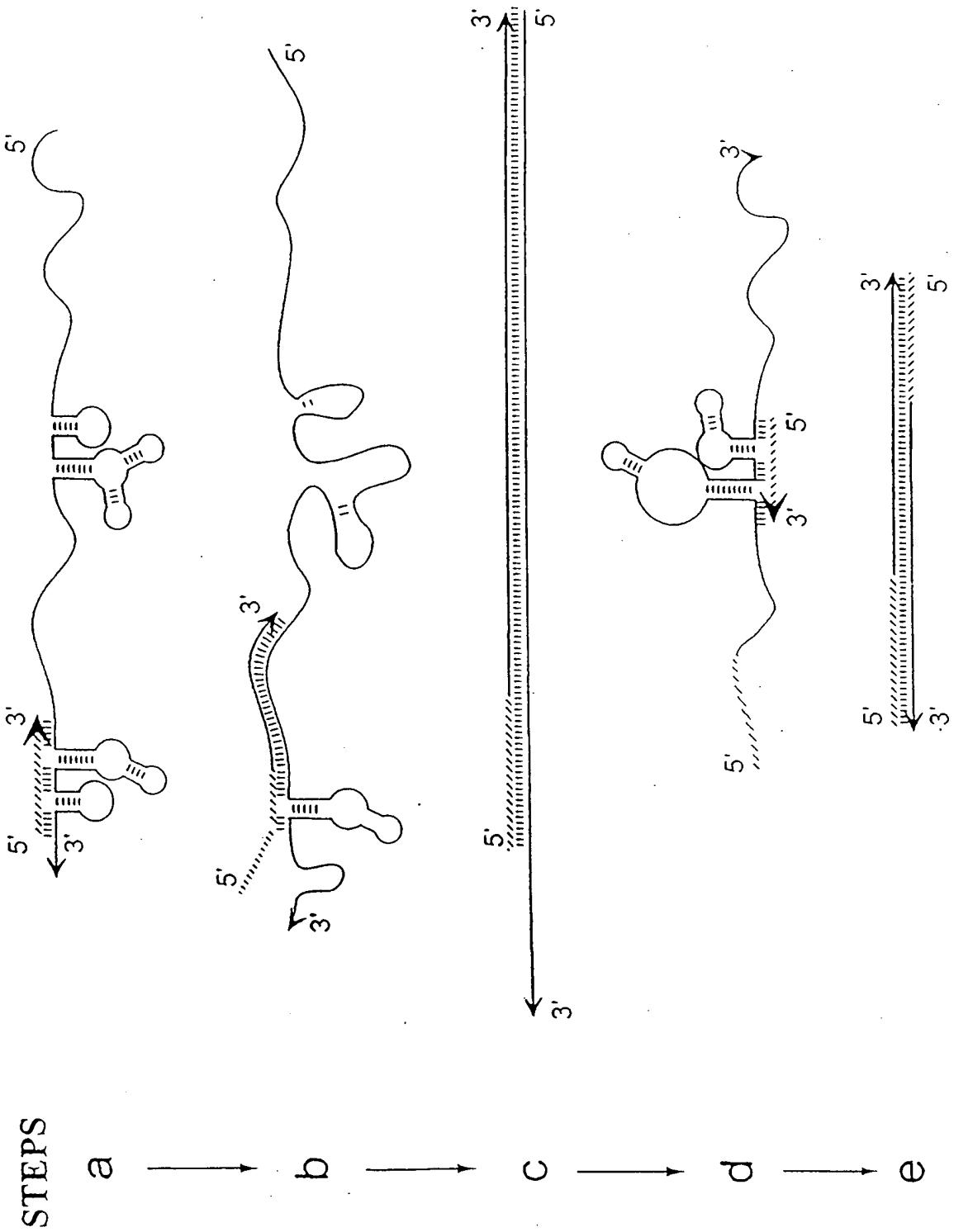


FIGURE 34

STEPS



STEPS

FIGURE 35

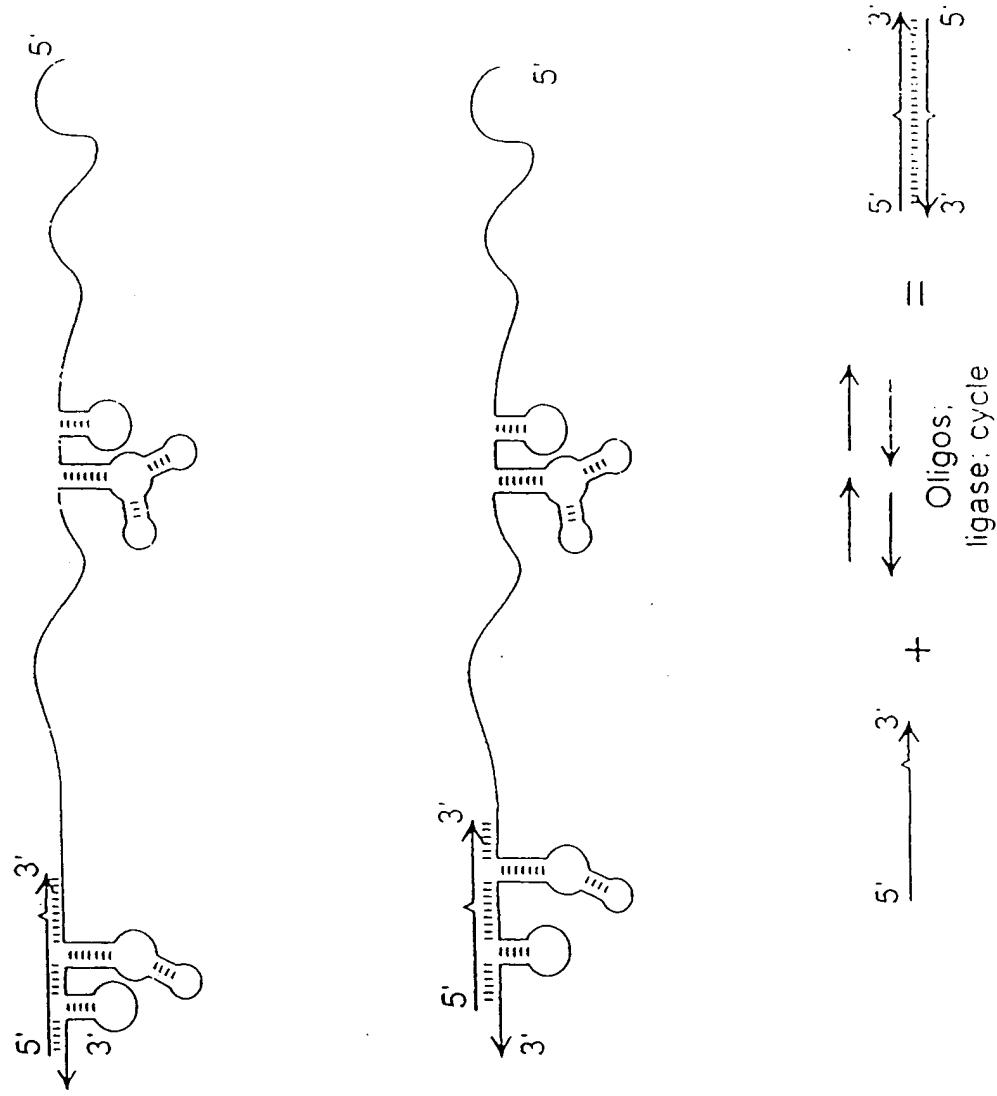


FIGURE 36

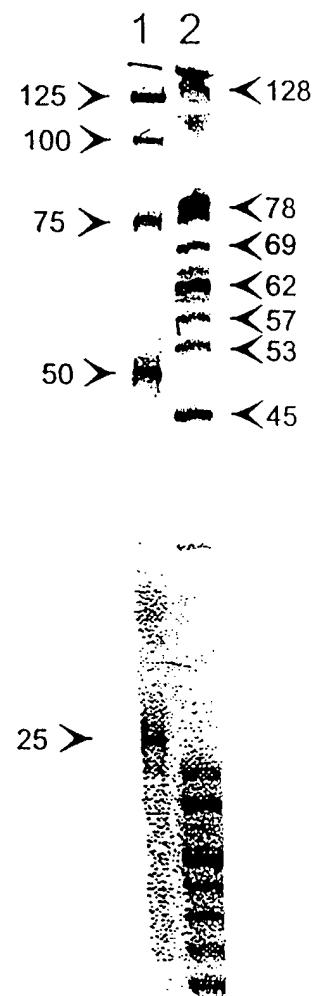


FIGURE 37A

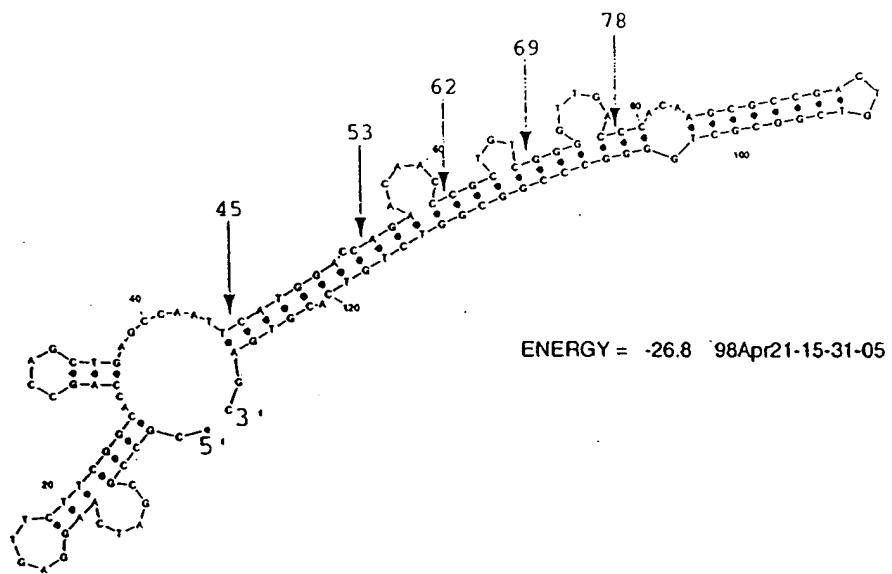
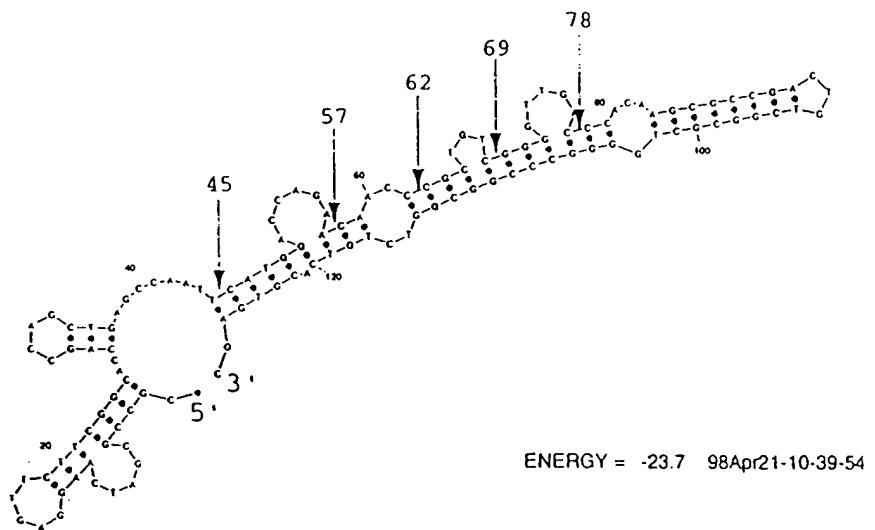


FIGURE 37B

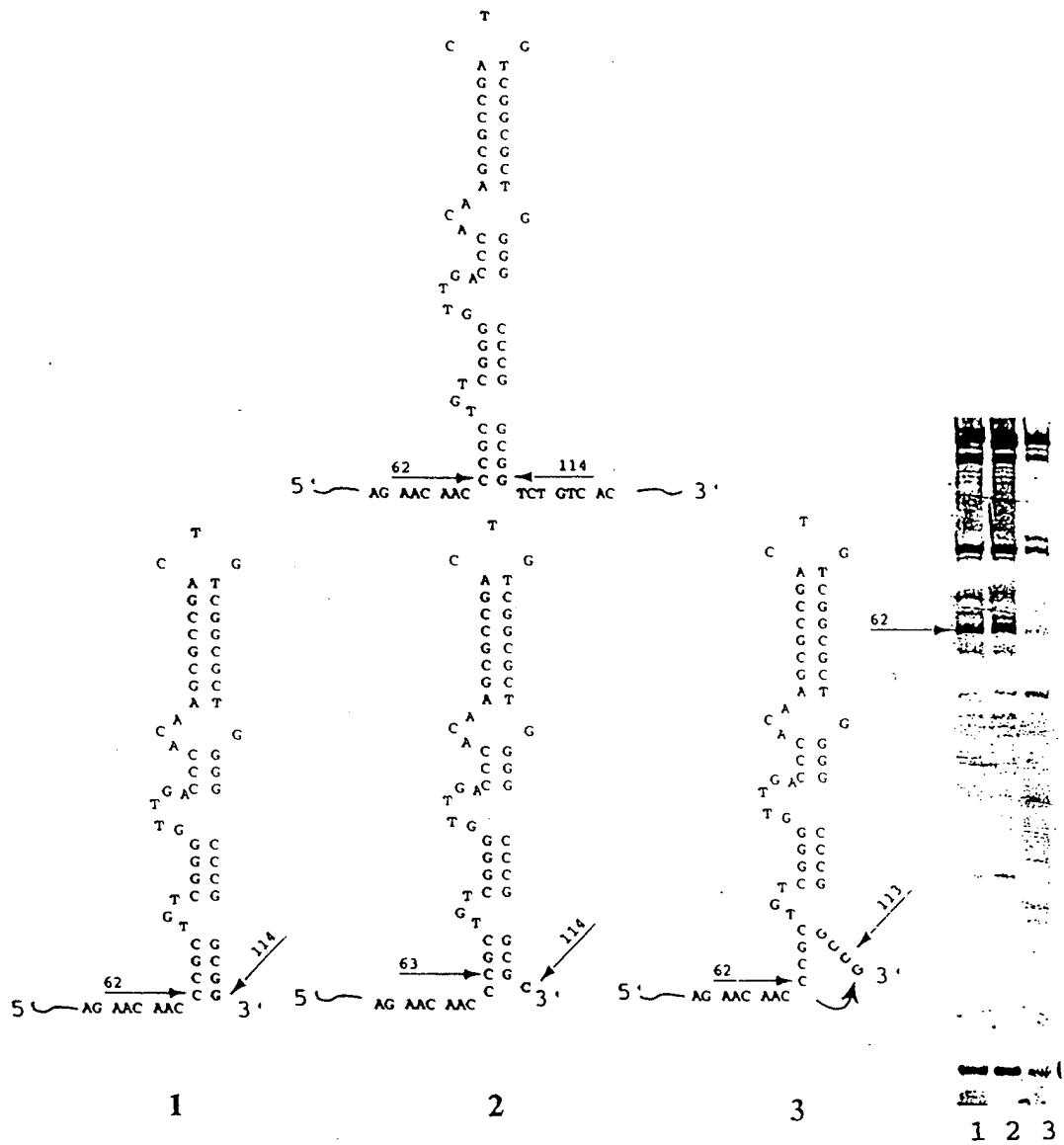


FIGURE 37C

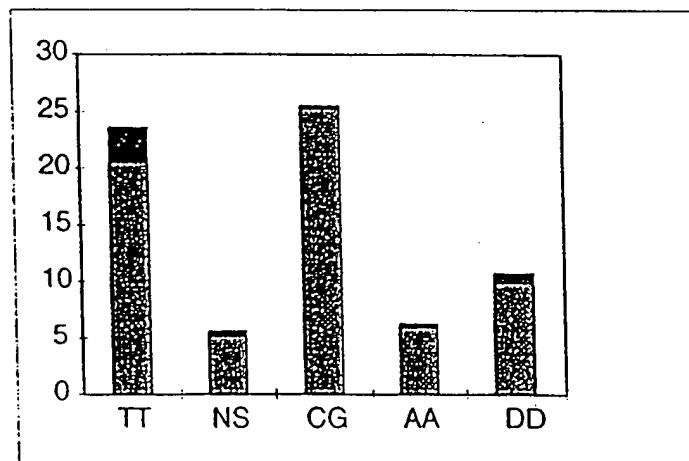
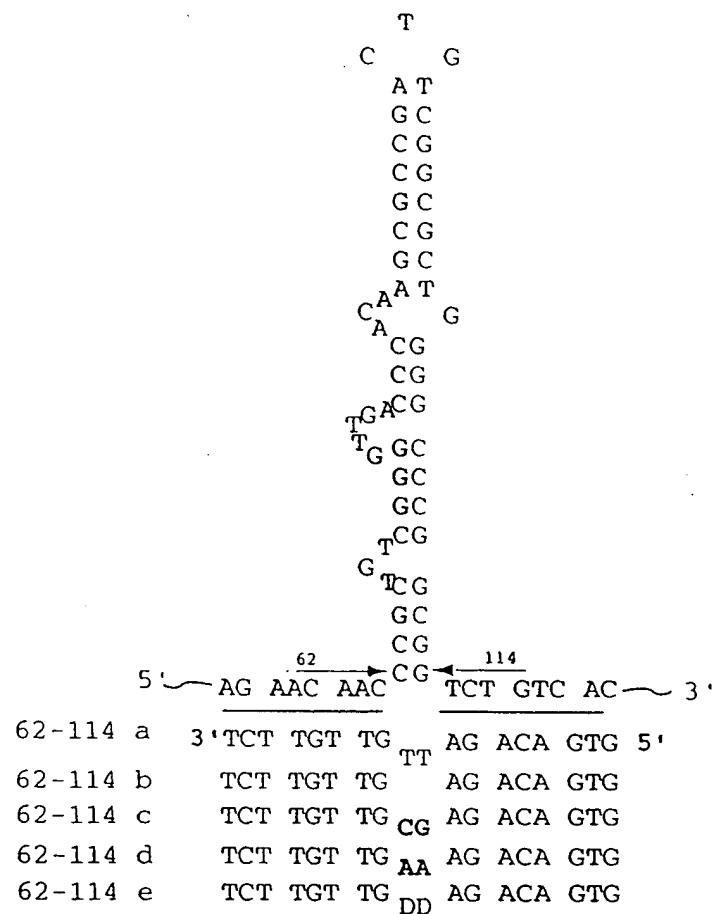


FIGURE 38A

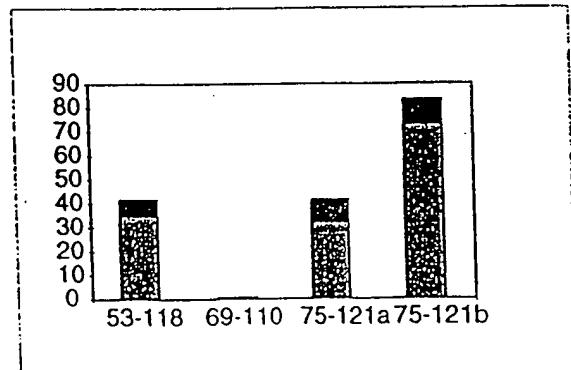
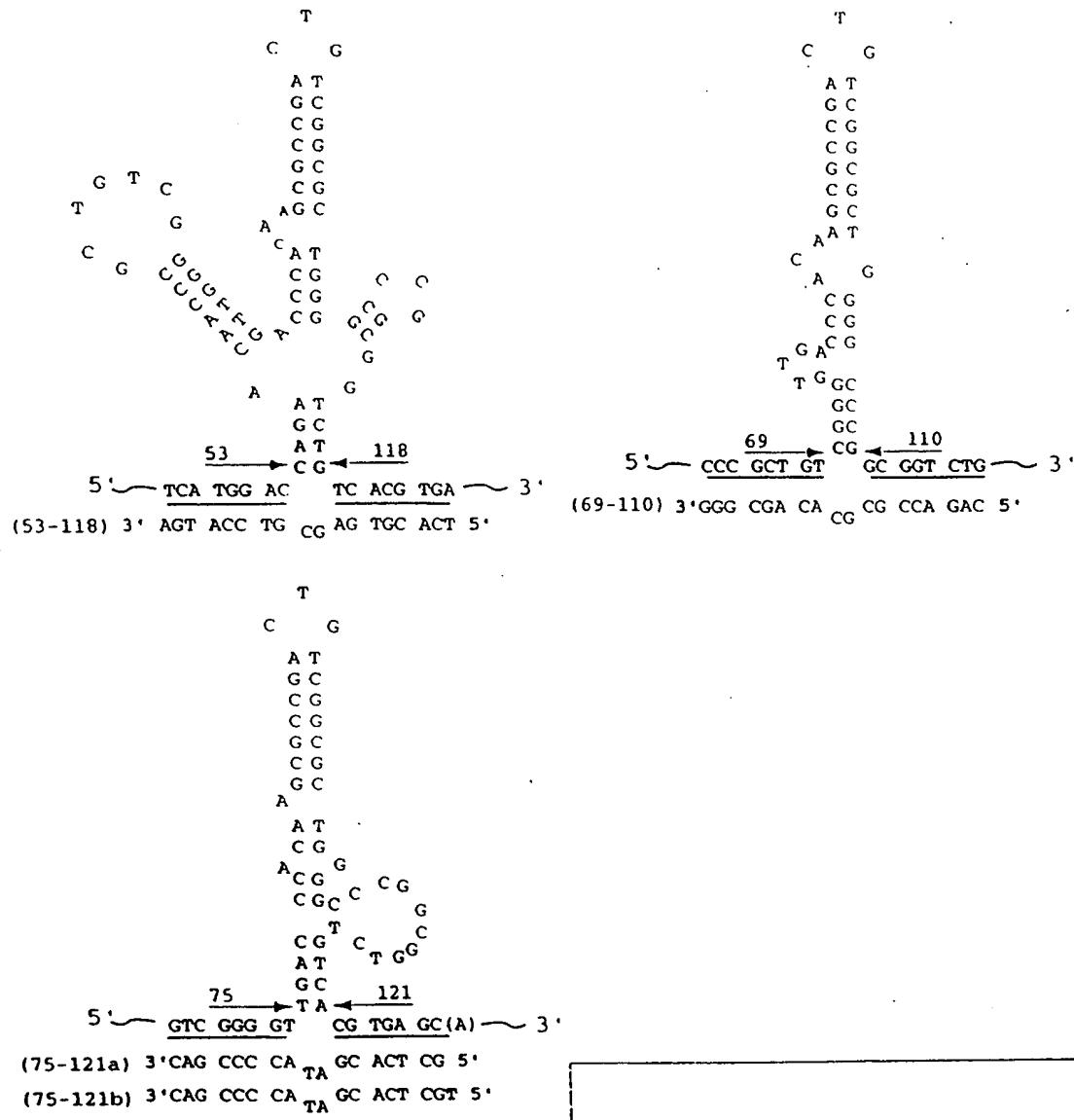


FIGURE 38B

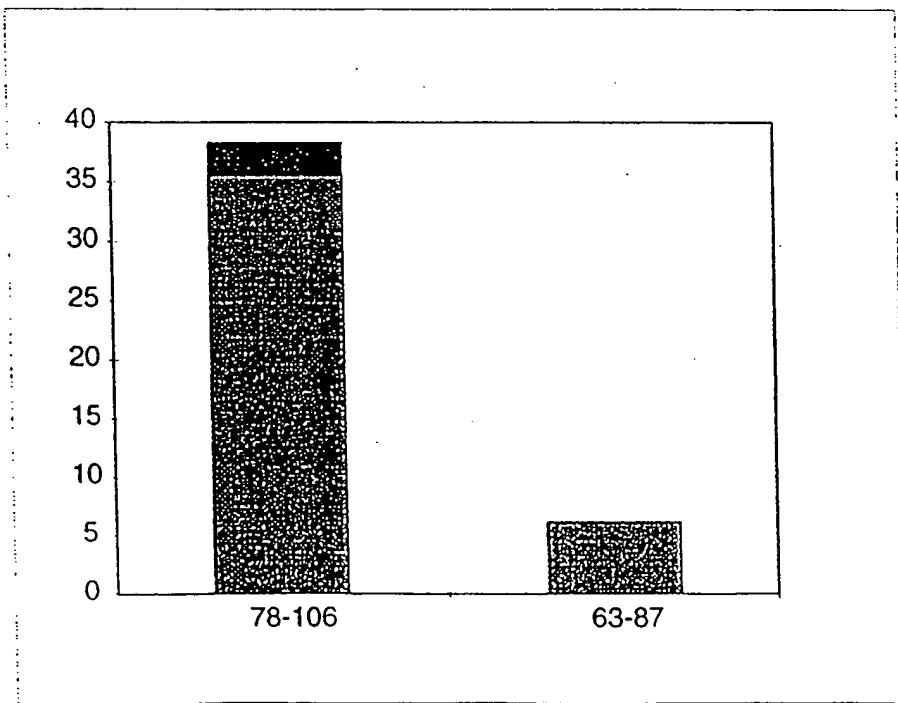
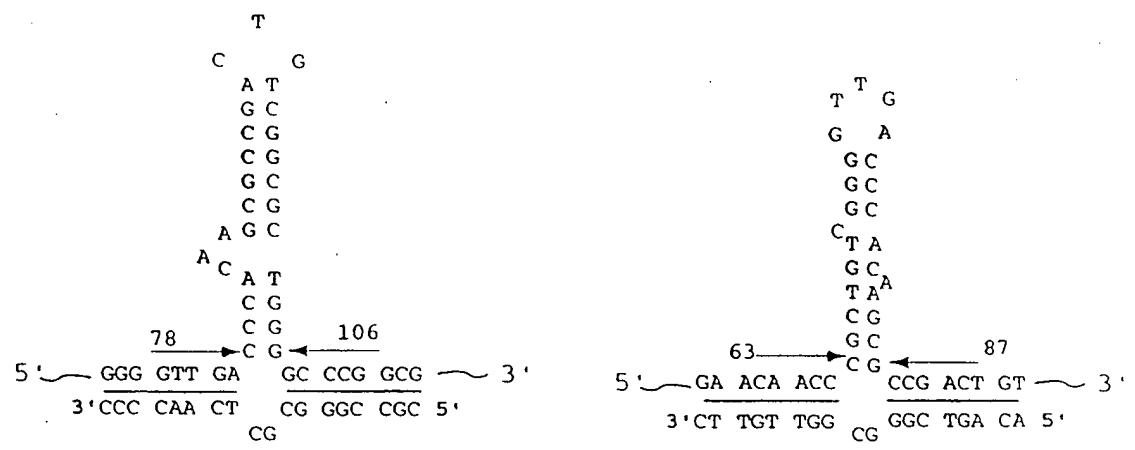


FIGURE 38C

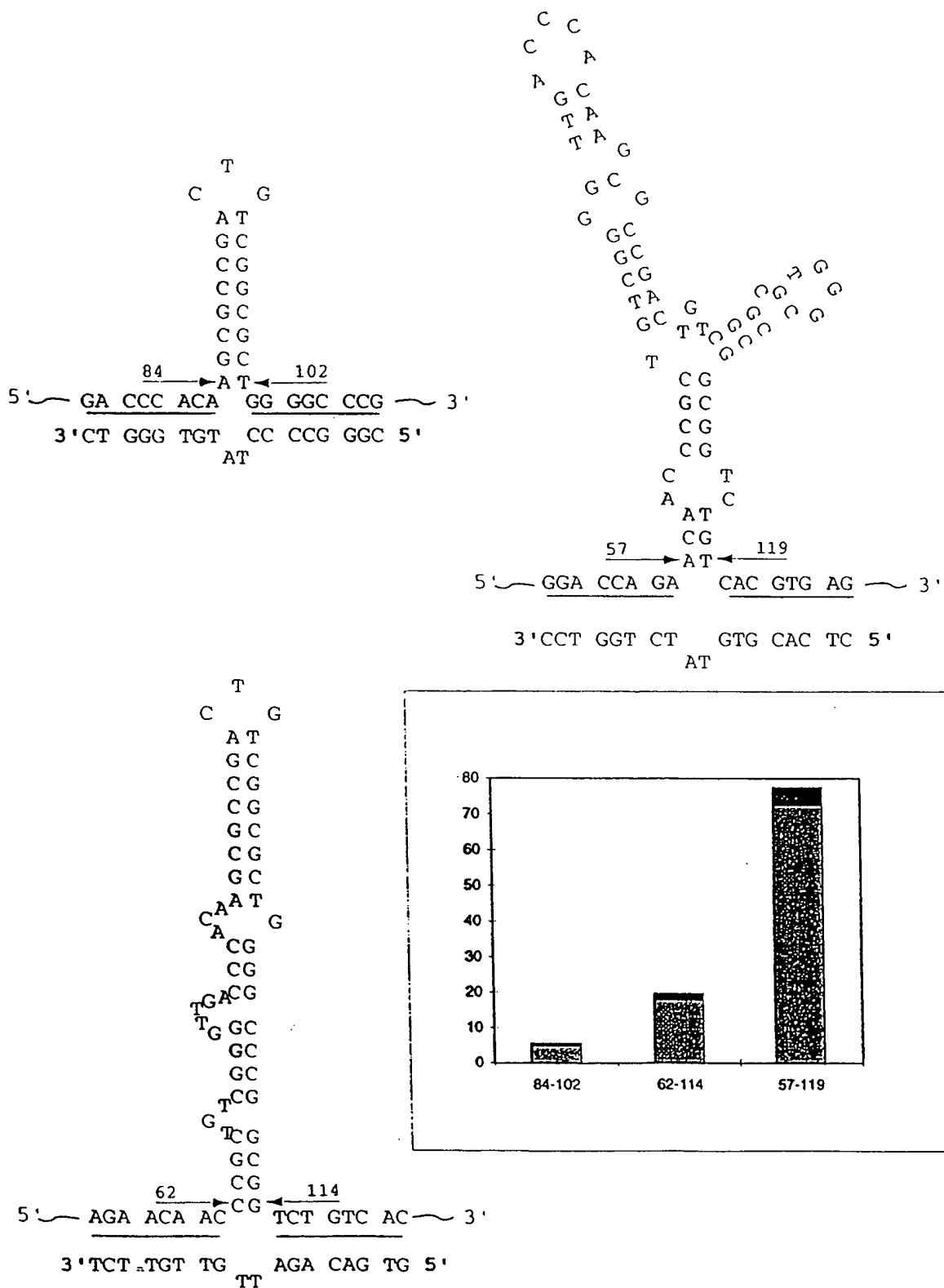


FIGURE 39

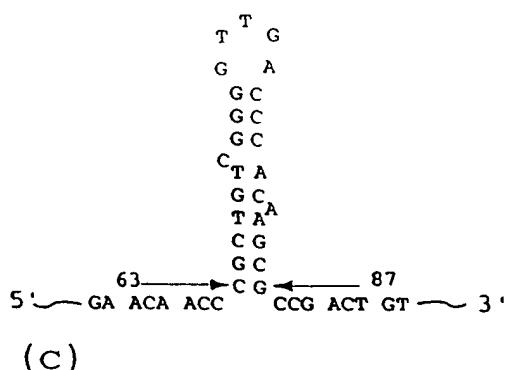
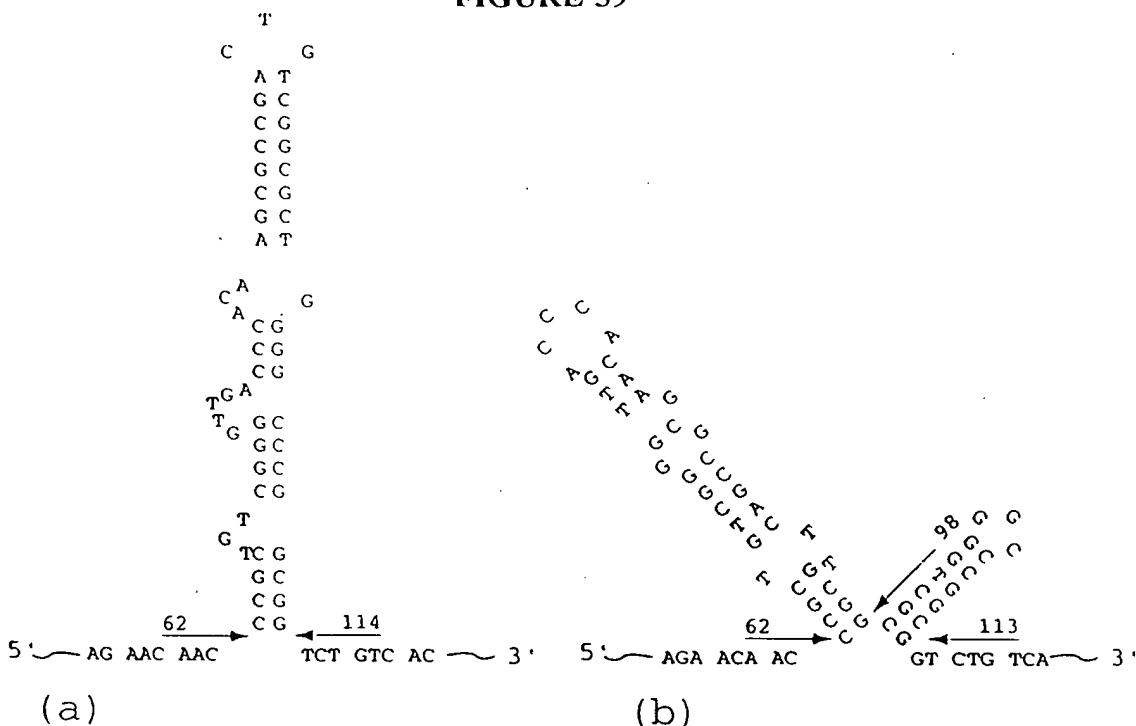


FIGURE 40

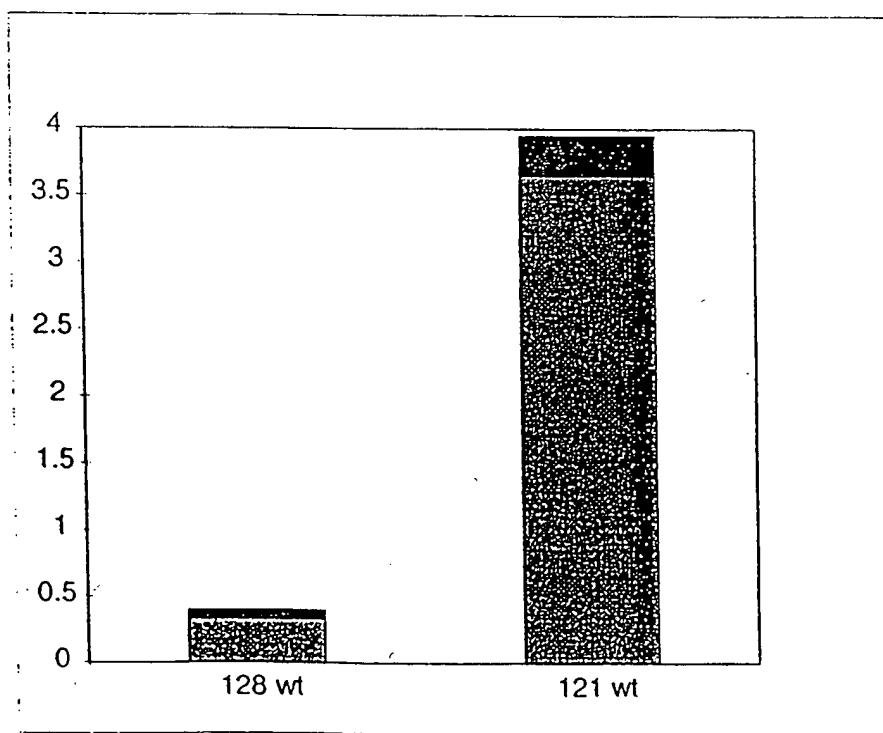
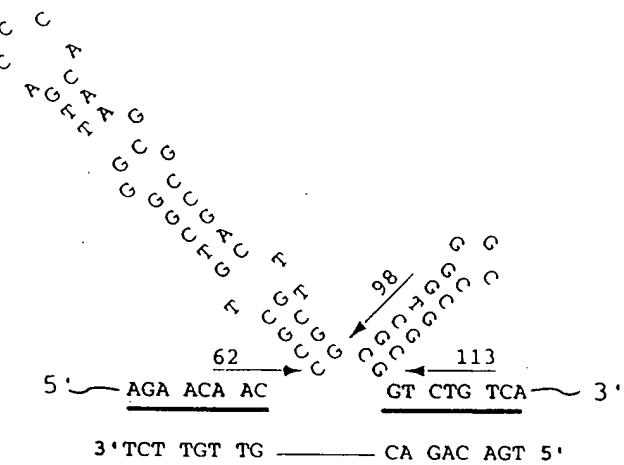


FIGURE 41

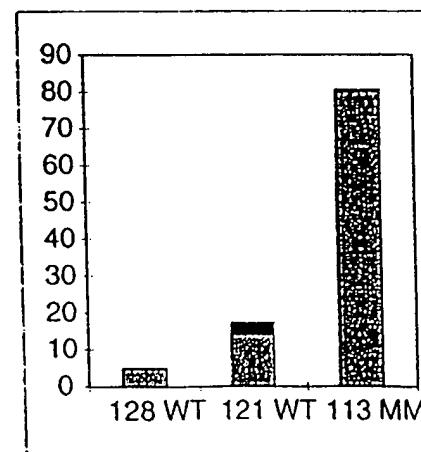
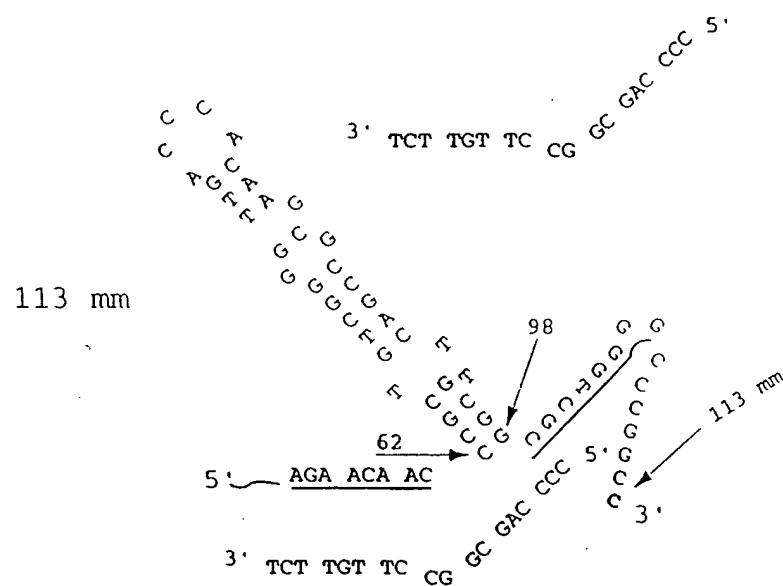
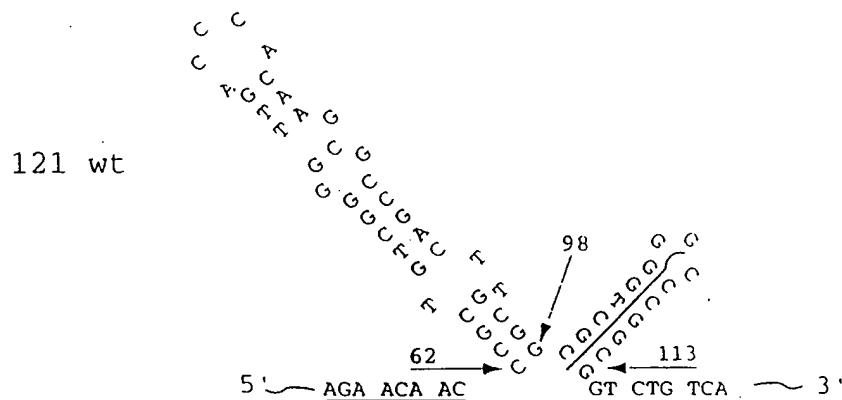


FIGURE 42

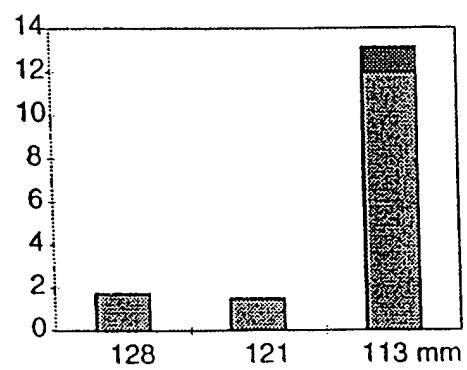
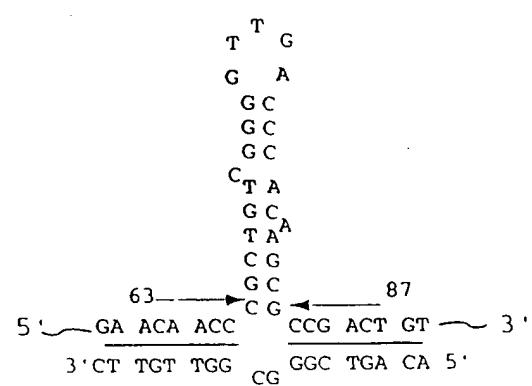


FIGURE 43A

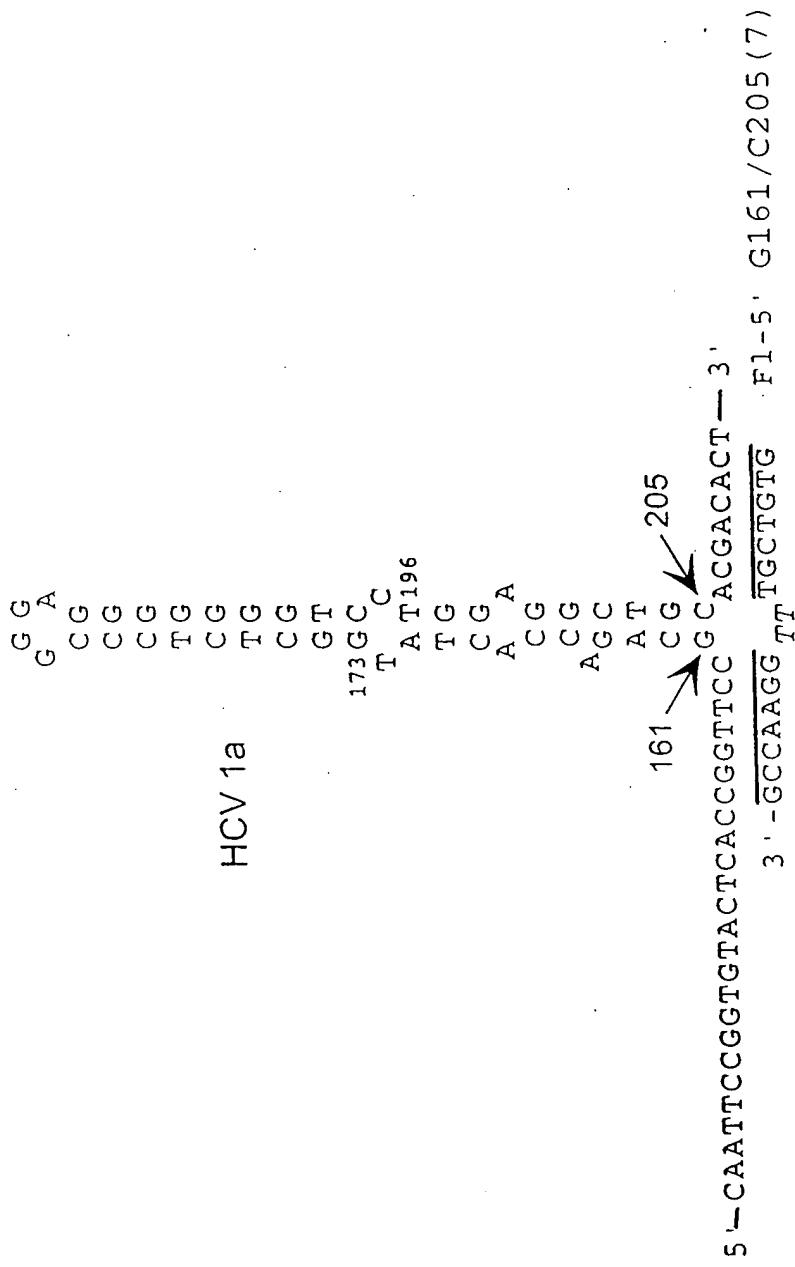


FIGURE 43B

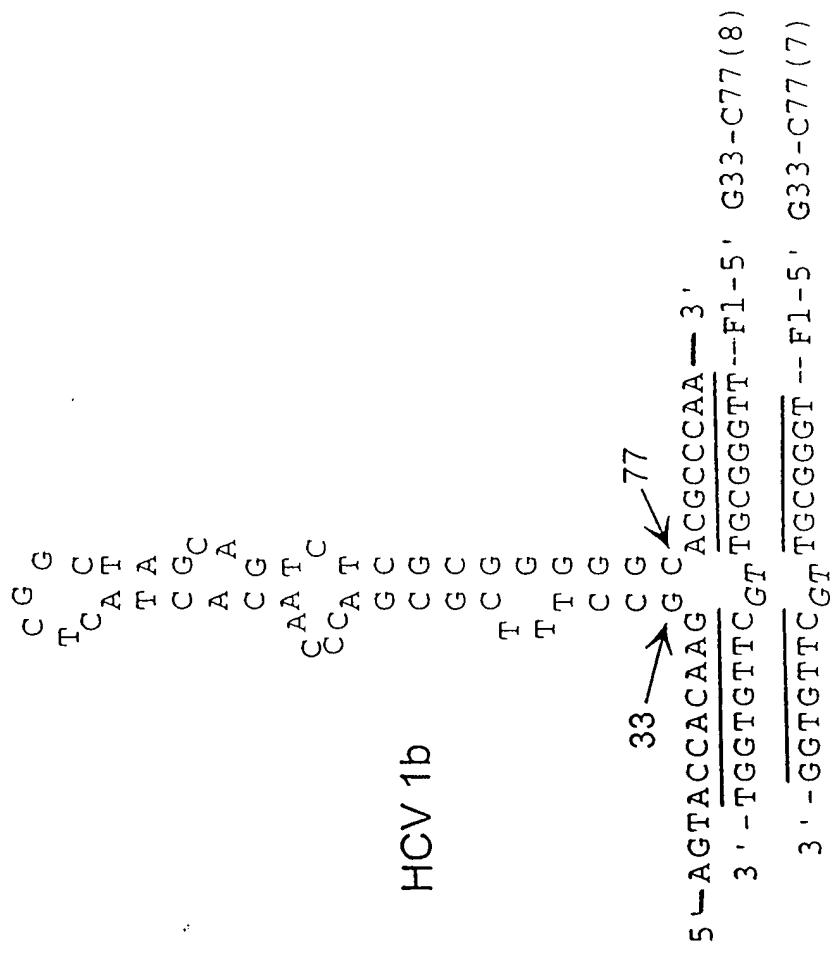


FIGURE 44A

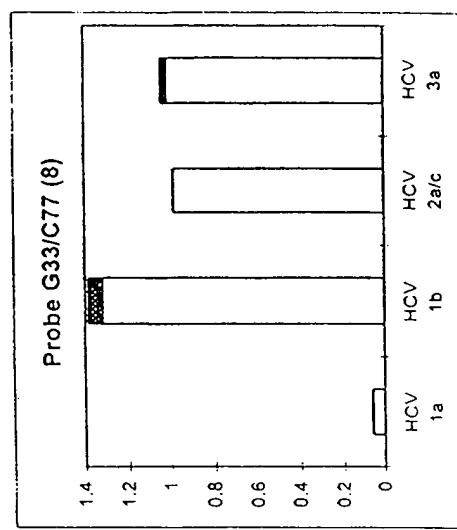
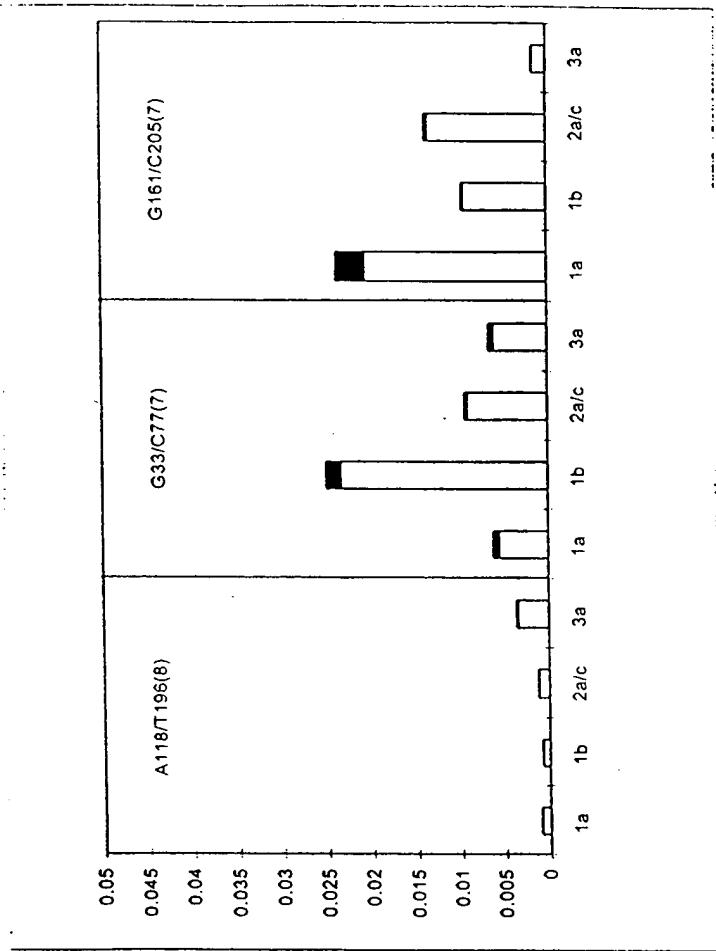


FIGURE 44B



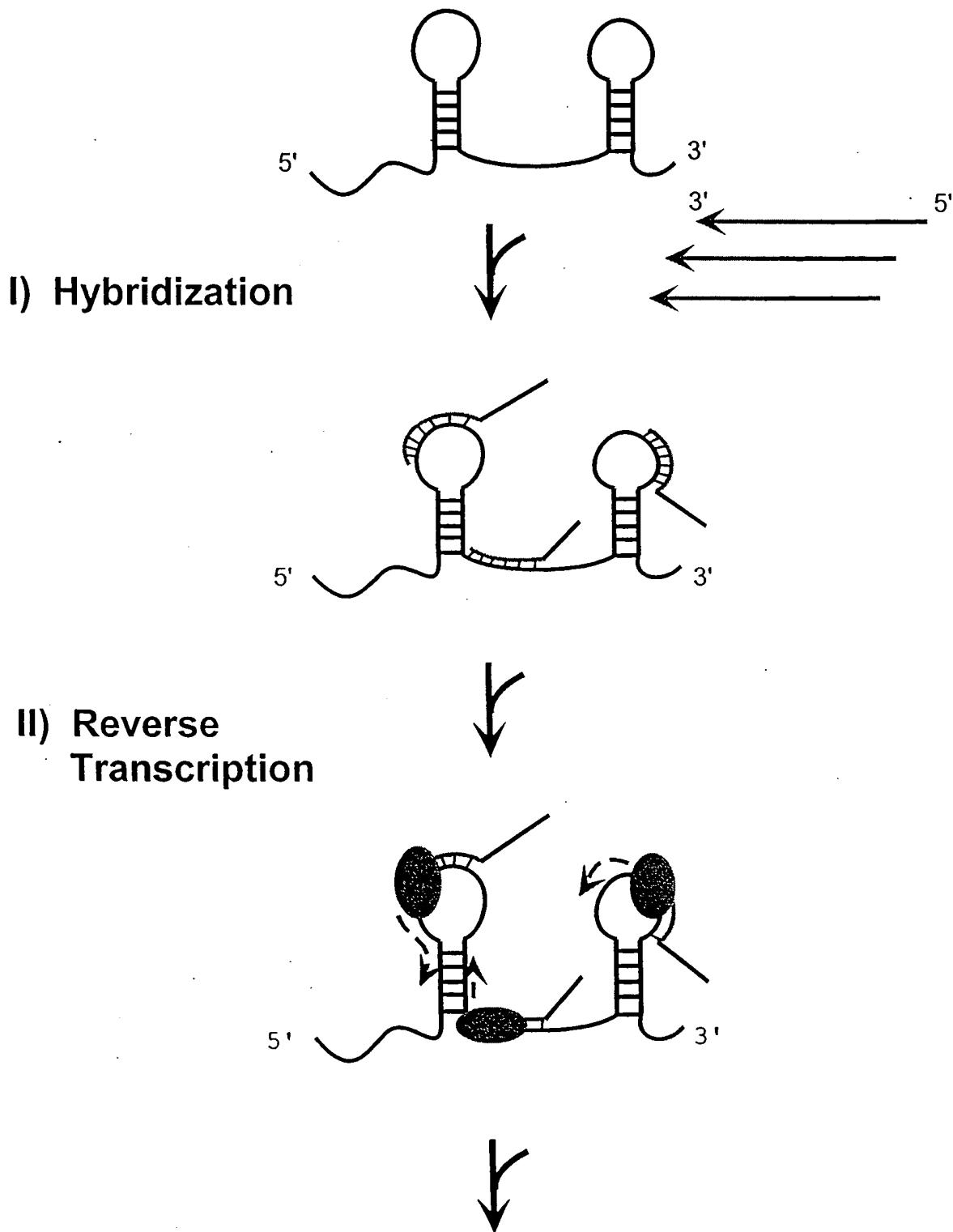
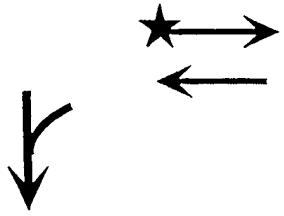
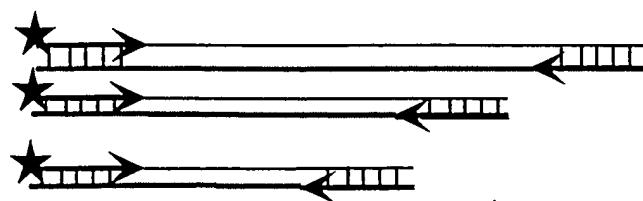


FIGURE 45A



III) PCR



IV) PAGE with Sequencing Ladder

A C G T RT-Products

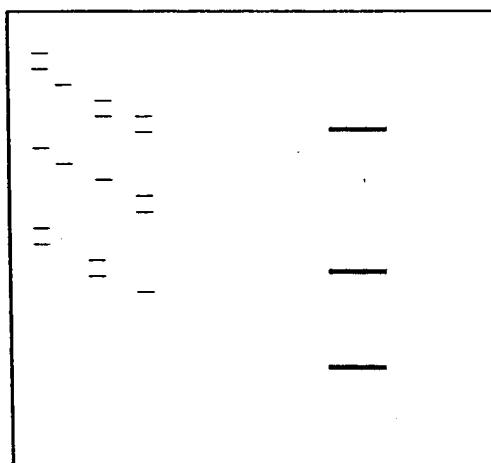
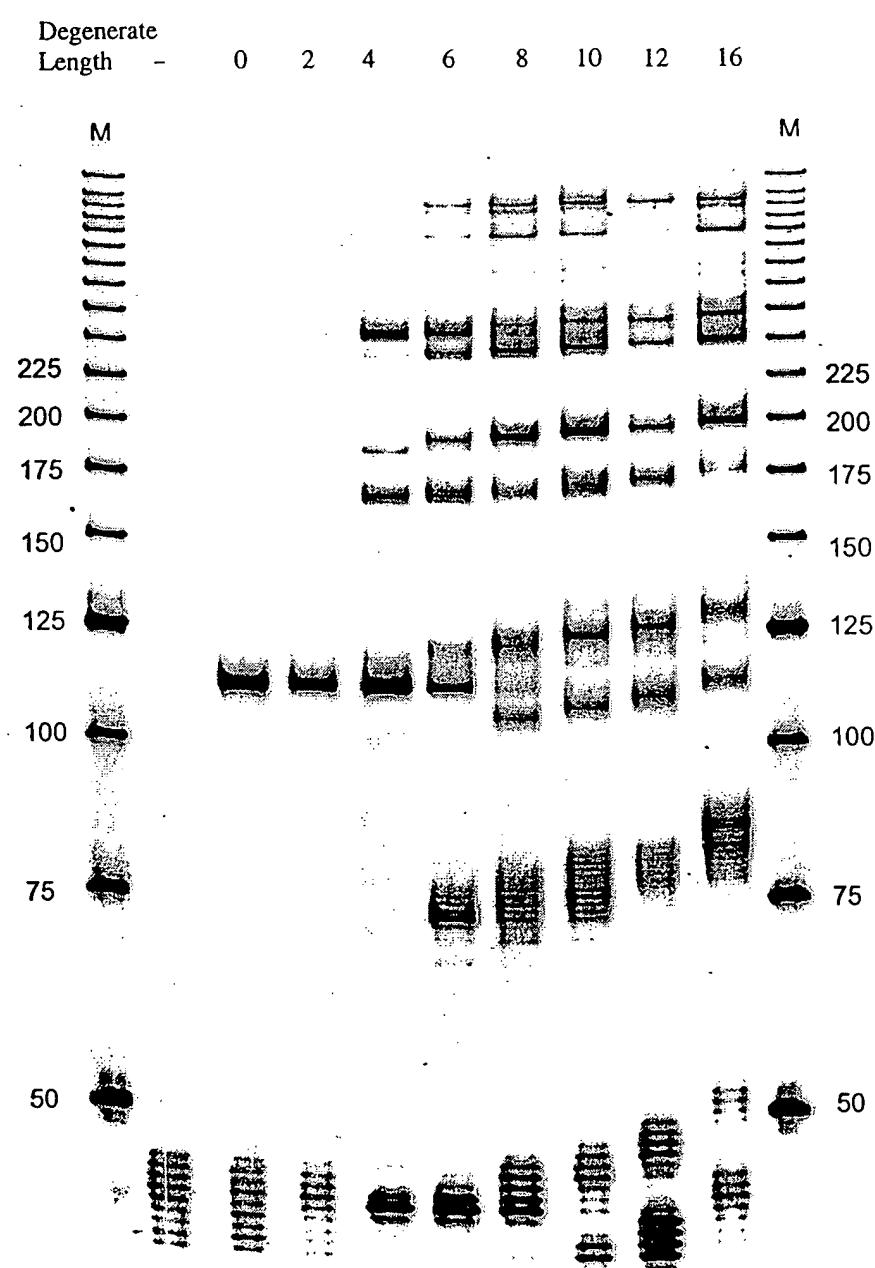


FIGURE 45B

FIGURE 46



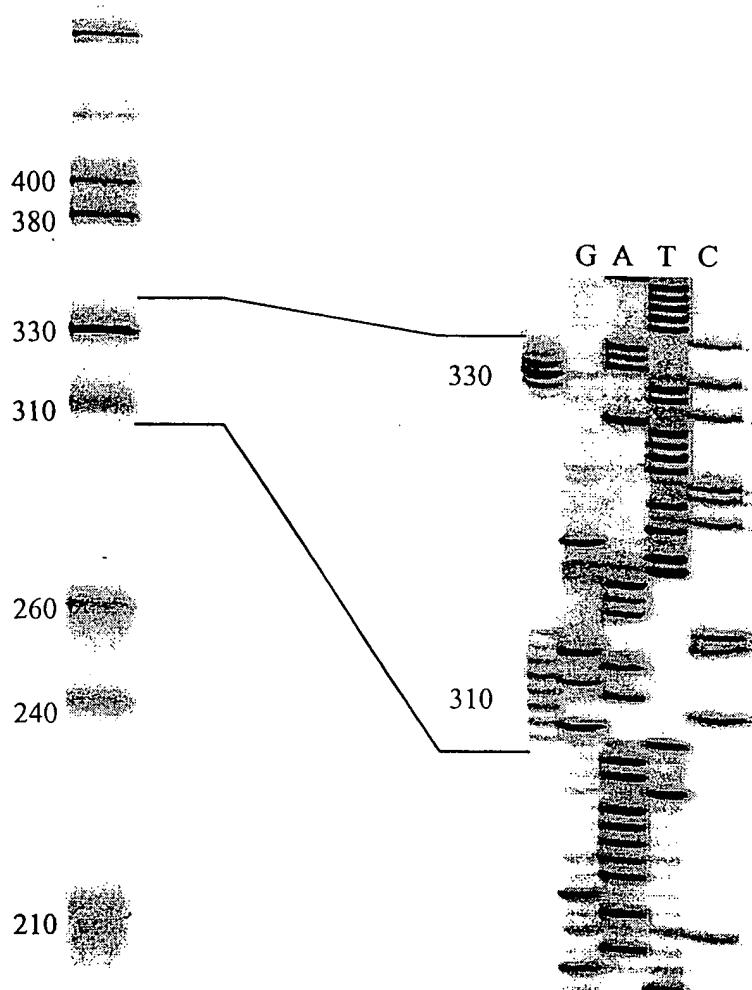
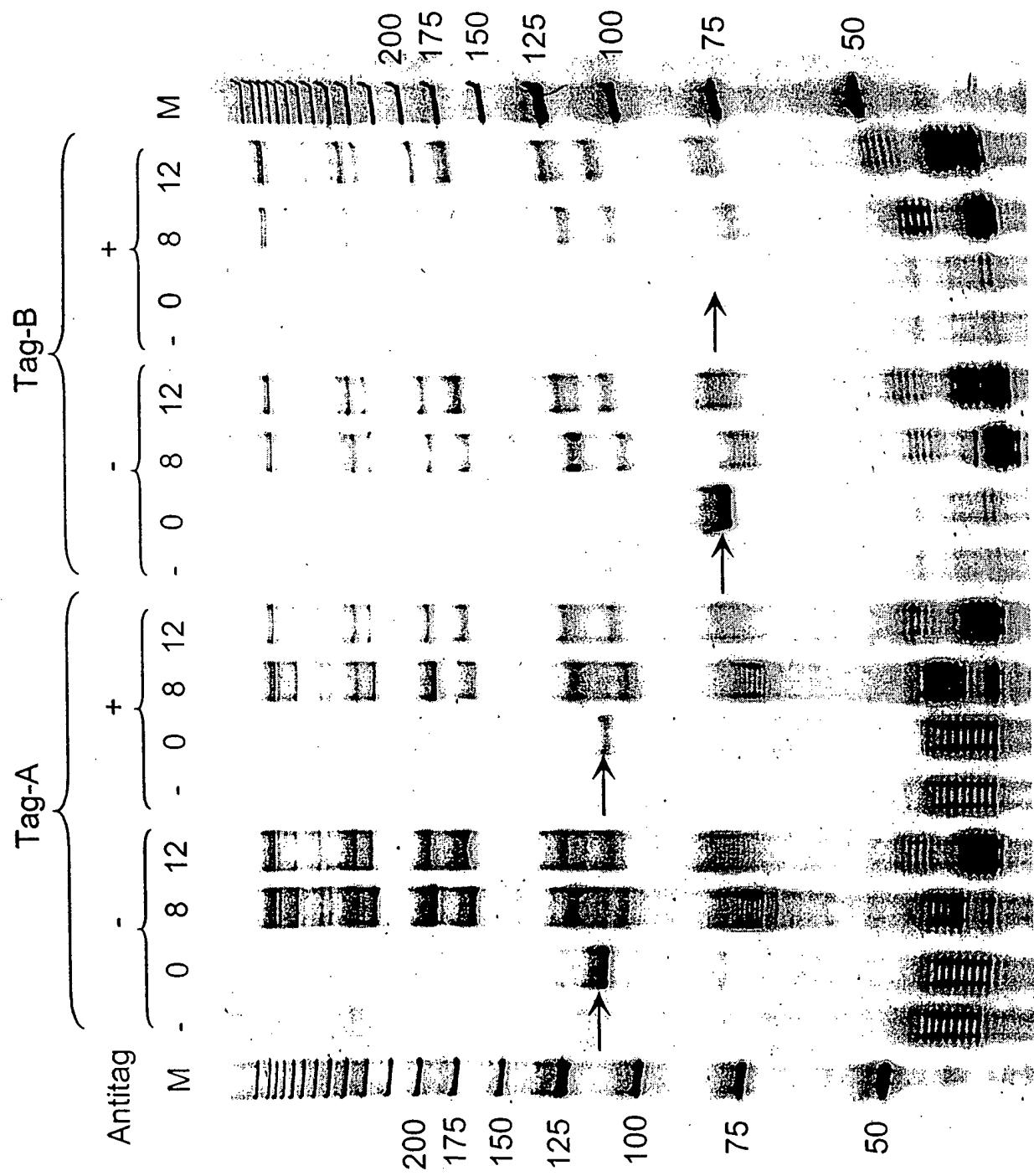


FIGURE 47

FIGURE 48



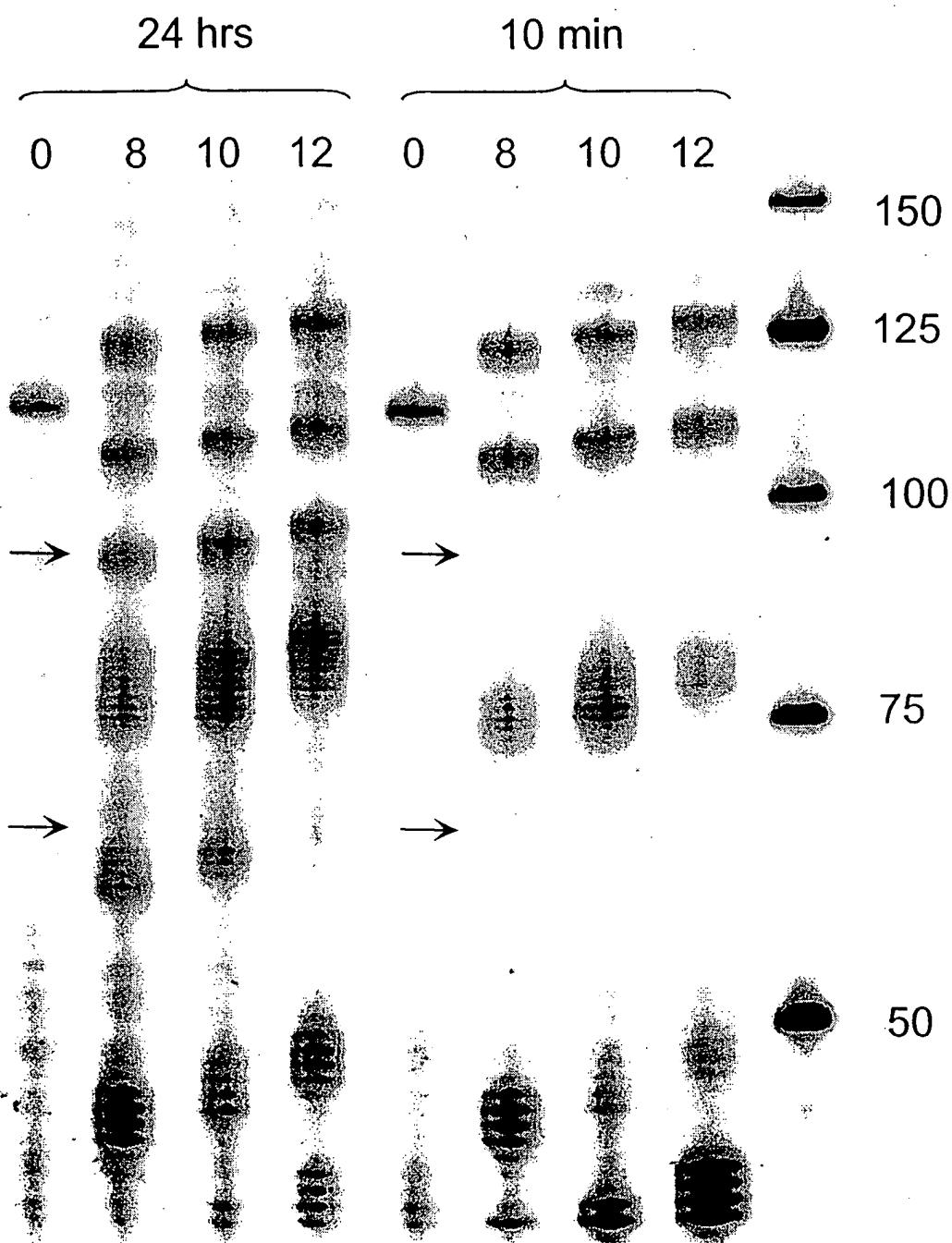


FIGURE 49

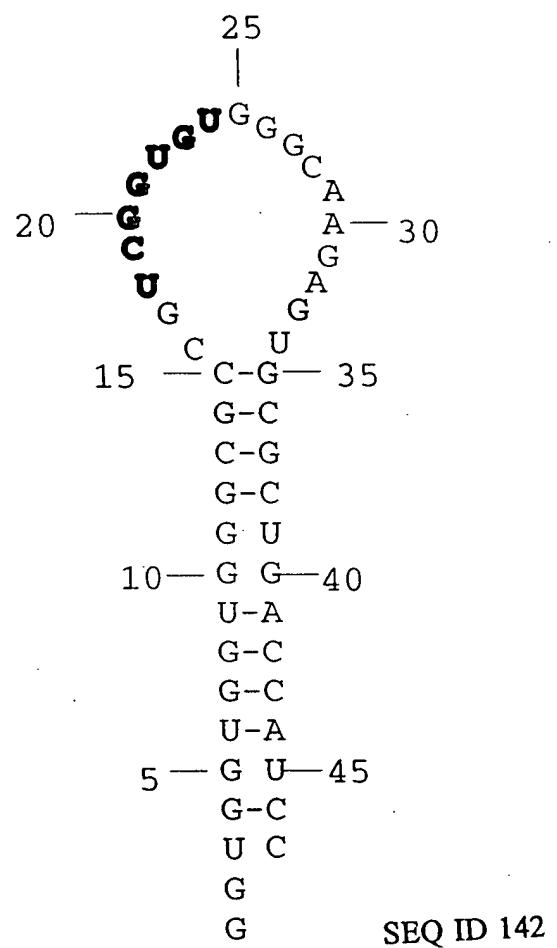


FIGURE 50A

FIGURE 50B

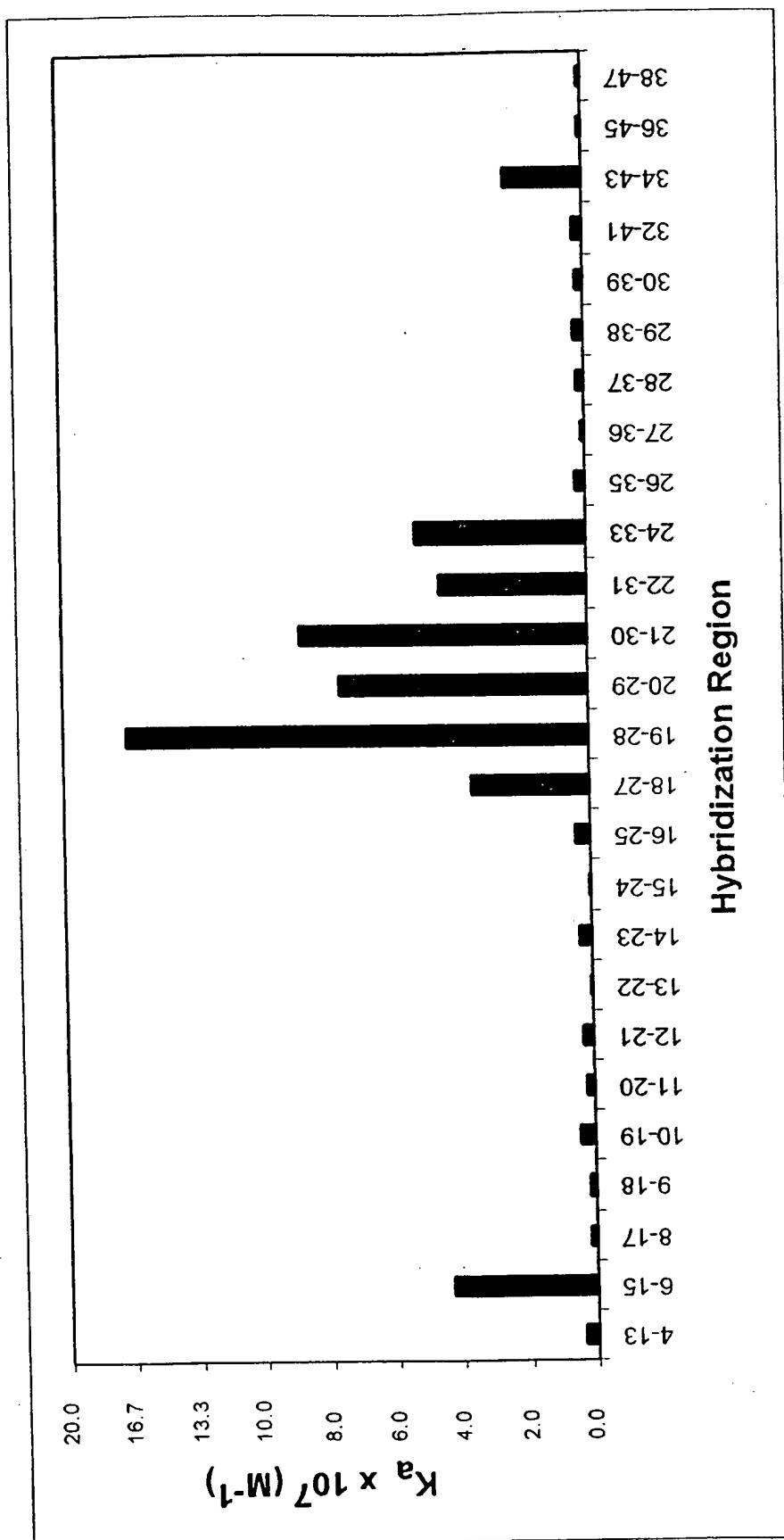


FIGURE 51

44-50

1 ACACUUGC_{UU} UUGACACAAC UGUGUUUACU UGC_{AA}UCCCC CAAAACAGAC

64-68

51 AGA_AU_GGGUGC AUCUGUCCAG UGAGGAGAAG UCUGCGGUCA CUGCCCUGUG

88-97

101 GGGCAAGGUG AAUGUGGAAG AAGUUGGUGG UGAGGCCUG GGCAGGCUGC

151 UGGUUGUCUA CCCAUGGACC CAGAGGUUCU UCGAGUCCUU UGGGGACCUG

FIGURE 52A

ISIS 1571 (-) ISIS 3067(+)

1 GCGCCCCAGT CGACGCTGAG CTCCTCTGCT ACTCAGAGTT

ISIS 1570 (+)

41 GCAACCTCAG CCTCGCTATG GCTCCCAGCA GCCCCCCGGCC

81 CGCGCTGCC GCACTCCTGG TCCTGCTCGG GGCTCTGTTC

121 CCAGGACCTG GCAATGCCCA GACATCTGTG **TCCCCCTCAA**

161 AAGTCATCCT GCCCCGGGGA GGCTCCGTGC TGGTGACATG

201 **CAGCACCTCC** TGTGACC**AGC CCAAGTTGTT GGGCATAGAG**

241 **ACCCCGTTGC** CTAAAAAGGA GTTGCTCCTG CCTGGGAACA

281 ACCGGAAGGT GTATGAACTG AGCAATGTGC AAGAAGATAG

ISIS 1934 (-)

321 CCAACCAATG TGCTATTCAA ACTGCCCTGA TGGGCAGTCA

361 ACAGCTAAAA CCTTCCTCAC CGTGTACTGG ACTCCAGAAC

401 GGGTGGAACT GGCACCCCTC CCCTCTTGGC AGCCAGTGGG

441 CAAGAACCTT ACCCTACGCT GCCAGGTGGA GGGTGGGGCA

481 **CCCCGGGCCA** ACCTCACCGT GGTGCTGCTC CGTGGGGAGA

FIGURE 52B

521 AGGAGCTGAA ACGGGAGCCA GCTGTGGGGG AGCCCGCTGA

as 610

561 GGTCACGACC ACGGTGCTGG TGAGGAGAGA TCACCATGGA

601 GCCAATTCT **CGTGC**CGC**AC** TGAACTGGAC CTGCGGCC**CC**

641 AAGGG**CTGG**A GCTGTTGAG AAC**ACCTCG**G CCCC**CTACCA**

681 GCTCCAGACC TTTGTCCTGC **CAGCG**ACTCC CCCACAACTT

721 GTCAGCCCCC GGGTCCTAGA GGTGGACACG CAGGGGACCG

761 TGGTCTGTTC **CTGGACGGG** CTGTTCCCAG TCT**CGGAGGC**

801 CCAGGTCCAC CTGGCACTGGACTGG GGGACCAGAG GTTGAACCCC

841 ACAGTCACCT ATGGCAACGA CTCCTTCTCG GCCAAGGC**CT**

881 CAGTCAGTGT GACCGCAGAG GACGAGGGCA CCCAGCGG**CT**

921 GACGTGTGCA GTAATACTGG GGAACCAGAG CCAGGAGACA

961 CTGCAGACAG **TGACCATCTA** CAGCTTCCG GCGCC**AAACG**

1001 TGATTCTGAC GAAGCCAGAG GTCTCAGAAG GGACCGAGGT

FIGURE 52C

1041 GACAGTGAAG **TGTGAGGCC** ACCCTAGAGC CAAGGTGACG

1081 CTGAATGGGG TTCCAGCCCA GCCACTGGGC CCGAGGGCCC

1121 AGCTCCTGCT GAAGGCCACC CCAGAGGACA **ACGGGCGCAG**

1161 CTTCTCCTGC TCTGCAACCC TGGAGGTGGC CGGCCAGCTT

as 1220 (+)

1201 **ATACACAAGA** ACCAGACCCG **GGAGCTCGT** GTCCTGTAT**G**

1241 **GCCCCGACT** GGACGAGAGG GATTGTCCGG GAAACTGGAC

1281 GTGCCAGAA AATTCCCAGC **AGACTCCAAT** GTGCCAGGCT

1321 TGGGGAACC CATTGCCGA GCTCAAGTGT CTAAAGGATG

ISIS 1547 (+)

1361 GCACTTCCC ACTGCCATC **GGGAATCAG** TGACTGTCAC

1401 TCGAGATCTT **GAGGGCACCT** ACCTCTGTCG GGCCAGGAGC

1441 ACTCAAGGGG AGGTACCCG CGAGGTGACC GTGAATGTGC

1481 TCTCCCCCG GTATGAGATT GTCATCATCA CTGTGGTAGC

1521 AGCCGCAGTC **ATAATGGCA** CTGCAGGCCT **CAGCACGTAC**

FIGURE 52D

1561 CTCT**ATAACC** GCCAGCGGAA GATCAAGAAA TACAGACTAC

as 1630 as 1630h (+++)

1601 **AACAGGCCCA** AAAAGGGACC CCCATGAAAC **CGAACACACA**

ISIS 1938 (+)

1641 **AGCCAC** GCCT CCCTGAACCT ATCCCGGGAC **AGGGCCTCTT**

1681 **CCTCGGCCTT** CCCATATTGG TGGCAGTGGT **GCCACACTGA**

1721 ACAGAGTGGA AGACATATGC CATGCAGCTA CACCT**ACCGG**

1761 **CCCTGGGACG** CCGGAGGACA GGGCATTGTC CTCAGTCAGA

1801 TACAACAGCA TTTGGGGCCA TGGTACCTGC **ACACCTAAAA**

1841 CACT**AGGCCA** CGCATCTGAT CTGTAGTCAC ATGACTAAGC

1881 CAAGAGGAAG **GAGCAAGACT** CAAGACATGA TTGATGGATG

ISIS 1939 (+)

1921 TTAAAGTCTA GCCTGATG**AG** AGGGGAAGTG GTGGGGGAGA

1961 CATAGCCCCA CCAT**GAGGAC** ATACAACTGG GAAATACTGA

2001 AACTTGCTGC CTATTGGTA TGCT**GAGGCC** CACAGACTTA

2041 CAGAAG**AGT** GGCCCTCCAT AGACATGTGT AGCATCAAAA

FIGURE 52E

ISIS 2302 (+)
2081 CACAAAGGCC CACACTCCT GACGGATGCC AGCTTGGGCA

2121 CTGCTGT**CTA** CTGACC**CCAA** CCCTTGATGA TATGTATTAA

ISIS 1572
2161 TTCATTGTT ATT**TTACCAG** CTATTTATTG AGTGTCTTTT

2201 ATGTAGGCTA AATGAACATA GGTCTCTGGC CTCACGGAGC

2241 TCCCAGTCCA TGTCACATTC AAGGTCACCA GGTACAGTTG

2281 TACAGGTTGT ACACTGCAGG AGAGTGCCTG GCAAAAAGAT

2321 CA**AATGGGGC** TGGGACTTCT CATTGGCCAA CCTGCCTTTC

2361 CCCAGAAGGA GTGATTTTC TAT**CGGCACA** AAAGCACTAT

2401 ATGGACTGGT AATGGTCAC AGGTCAGAG ATTACCC**AGT**

2441 **GAGGCCTTAT** TCCTCC**CTTC** CCCCCAAAAC TGACACCTTT

2481 GT**TAGCCACC** TCCCC**ACCA** CATACTTTC TGCCAGTGT

2521 CACAATGACA CTCAGCGGTC ATGTCTGGAC ATGAGTGC

2561 AGGGA**ATATG** CCCAAGCTAT GCCTTGTCT CTTGTCTGT

FIGURE 52F

2601 TTGCATTTCA CTGGGAGCTT GCACTATTGC AGCTCCAGTT

2641 TCCTGCAGTG ATCAGGGTCC TGCAAGCAGT GGGGAAGGGG

2681 GCCAAGGTAT TGGAGGACTC CCTCCCAGCT TTGGAAGGGT

2721 CATCCCGCGTG TGTGTGTGTG TGTATGTGTA GACAAGCTCT

2761 CGCTCTGTCA CCCAGGCTGG AGTGCAGTGG TGCAATCATG

2801 GTTCACTGCA GTCTTGACCT TTTGGGCTCA AGTGATCCTC

2841 CCACCTCAGC CTCCTGAGTA GCTGGGACCA TAGGCTCACA

2881 ACACCACACC T

FIGURE 53A

1 CACAUUGUUC UGAUCAUCUG AAGAUCAGCU AUUAGAAGAG

41 AAAGAUCAGU UAAGUCCUUU GGACCUGAUC AGCUUGAUAC site 80

81 AAGAACUACU GAUUUCAACU UCUUJGGCUU AAUUCUCUCG site 120

121 GAAACGAUGA AAUAUACAAG UUUAUACUUG GCUUUUCAGC

161 UCUGCAUCGU UUUGGGUUCU CUUGGCUGUU ACUGCCAGGA

201 CCCAU AUGUA **CAAGAAGCAG** AAAACCUUAA GAAAUAUJUU site 210

241 AAUGCAGGGUC AUUCAGAUGU AGCGGAUAAU GGAACUCUUU site 240 site 260

281 UCUUAGGCAU UUUGAAGAAU UGGAAAGAGG AGAGUGACAG

321 AAAAAUAAUG **CAGAGCCAAA** UUGUCUCCUU UUACUUCAA site 330

361 CUUUUUAAAA ACUUUAAAAGA UGACCAGAGC AUCCAAAAGA site 380 site 400

401 GUGUGGAGAC CAUCAAGGAA GACAUGAAUG UCAAGUUUUU

441 CAAUAGCAAC AAAAAGAAAC GAGAUGACUU CGAAAAGCUG

FIGURE 53B

481 ACUAAUUAUU CGGUAACUGA CUUGAAUGUC CAACGCAAAG

site 560

521 CAAUACAUGA ACUCAUCCAA GUGAUGGCUG AACUGUCGCC

site 570

561 AGCAGCUAAA ACAGGGGAAGC GAAAAAGGAG UCAGAUGCUG

601 UUUCGAGGUC GAAGAGCAUC CCAGUAAUGG UUGUCCUGCC

641 UACAAUAUU GAAUUUAAA UCUAAAUCUA UUUAUUAAUA

681 UUUAACAUUA UUUUAUGGG GAAUUAUUU UUAGACUCAU

721 CAAUAAAUA AGUAUUUAUA AUAGCAACUU UUGUGUAAUG

761 AAAAUGAAUA UCUAUUAAUA UAUGUAUUAU UUAUAUUUCC

801 UAUAUCCUGU GACUGUCUCA CUUAAUCCUU UGUUUUCUGA

site 850

site 860

site 880

841 CUAAUUAGGC AAGGCUAUGU GAUUACAAGG CUUUAUCUCA

site 890

site 910

881 GGGGCCAACU AGGCAGCCAA CCUAAGCAAG AUCCCAUGGG

921 UUGUGUGUUU AUUUCACUUG AUGAUACAAU GAACACUUAU

961 AAGUGAAGUG AUACUAUCCA GUUACUA

FIGURE 54A

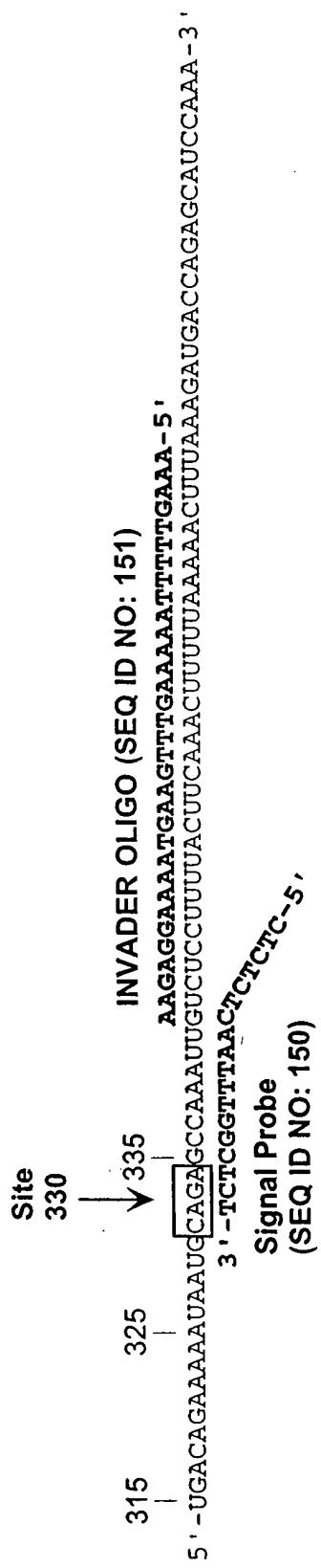


FIGURE 54B

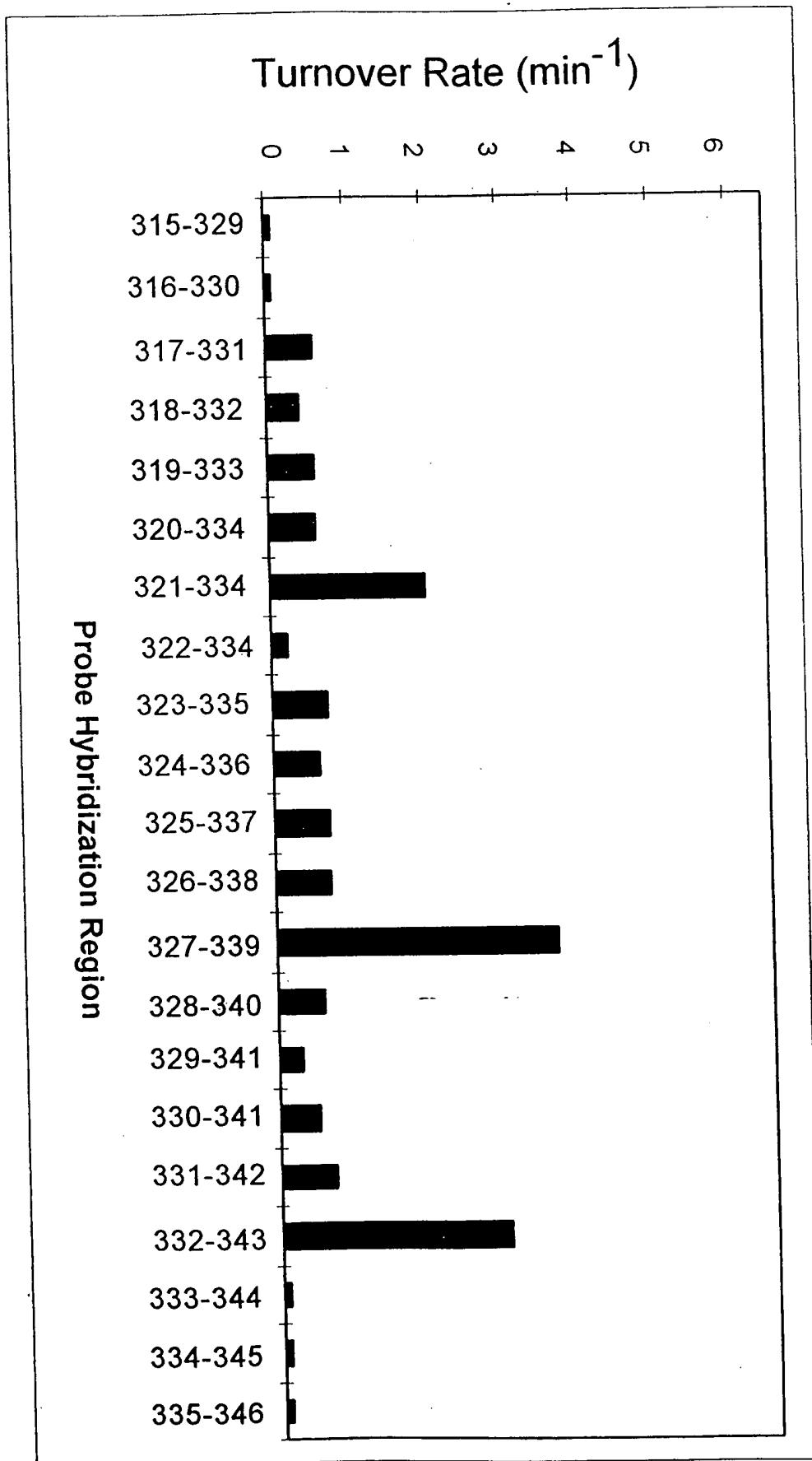


FIGURE 55A

SEQ ID NO:158

Primer 1

460 GGUCUCUCUG GUUAGACCAG AUCUGAGCCU GGGAGCUCUC UGGCUAACUA

510 GGGAAACCCAC UGCUUAAGCC UCAAUAAAGC UUGCCUUGAG UGCUUCAAGU

560 AGUGUGUGCC CGUCUGUUUGU GUGACUCUGG UAACUAGAGA UCCCUCAGAC

Primer 2

610 CCUUUUAGUC AGUGUGGAAA AUCUCUAGCA GUGGCGCCCG AACAGGGACC

660 UGAAAGCGAA AGGGAAACCA GAGGAGCUCU CUCGACGCAG GACUCGGCUU

710 GCUGAAGCGC GCACGGCAAG AGGCGAGGGG CGGCGACUGG UGAGUACGCC

760 AAAAUUUUG ACUAGCGGAG GCUAGAAGGA GAGAGAUGGG UGCGAGAGCG

Primer 3

810 UCAGUAUUAAC GCGGGGGAGA AUUAGAUCGA UGGGAAAAAA UUCGGUUAAG

860 GCCAGGGGGA AAGAAAAAAU AUAAAUAAGAA ACAUAUAGUA UGGGCAAGCA

910 GGGAGCUAGA ACGAUUCGCA GUUAAUCCUG GCCUGUUAGA AACAUCAAGAA

960 GGCUGUAGAC AAAUACUGGG ACAGCUACAA CCAUCCUUC AGACAGGAUC

Primer 4

1010 AGAAGAACUU AGAUCAUUAU AUAAAACAGU AGCAACCCUC UAUUGUGUGC

1060 AUCAAAGGAU AGAGAUAAAA GACAC**CCAAGG** AAGCUUUAGA CAAGAUAG**GAG**

FIGURE 55B

1110 **GAA**GAGCAAA ACAAAAGUAA GAAAAAAGCA CAGCAAGCAG CAGCUGACAC

1160 **AGG**ACACAGC AAUCAGGUCA GCCAAAAUUA CCCUAUAGUG CAGAACAUCC

Primer 5

1210 **AGGGGCAA**GU GGUACAUCAG GCCAUAUCAC CUAGAACUU AAAUGCAU

1260 GUAAAAGUAG UAGAAGAGAA GGCUUUCAGC CCAGAAGUGA UACCCAUGU

1310 UUCAGCAUUA UCAGA**AGGAG** **CC**ACCCCACA AGAUUUAAAC ACCAUGCUAA

1360 ACACAGUGGG GGGACAUCA **GC**AGCCAUGC AAAUGUUAAA AGAGACCAUC

Primer 6

1410 **AAU**GAAGGAAG CUGCAGAAUG GGAUAGAGUG CAUCCAGUGC AUGCAGGGCC

1460 UAUUGCAC**CA** GGCCAGAUGA GAGA**ACC**AAG **GG**GAAGUGAC AUAGCAGGAA

1510 CUACUAGUAC CCUUCAGGAA CAAAUAGGAU GGAUGACAAA UAAUCCACCU

1560 AUCCCAGUAG GAGAAAUUA UAAAAGAUGG AUAUCCUGG GAUAAAUA

Primer 7

1610 AAUAGUAAGA AUGUAUAGCC CUACCAGCAU UCUGGACAUA AGACAAGGAC

1660 CAAAGGAACC CUUUAGAGAC UAUGUAGACC GGUUCUAUAA AACUCUAAGA

1710 **GCCGAG**CAAG CUUC**ACAG**GA GGUAAAAAU **UGG**AUGACAG AAACCUUGUU

FIGURE 55C

1760 GGUCCAAAAU GCGAACCCAG AUUGUAAGAC UAUUUUAAAA GCAUUGGGAC

Primer 8

1810 **CAGCGGCUAC ACUAGAAGAA AUGAUGACAG CAUGUCAGGG AGUAGGAGGA**

1860 CCCGGCCAUA AGGCAAGAGU UUUGGCUGAA GCAAUGAGCC AAGUAACAAA

1910 UUCAGCUACC AUAAUGAUGC **AGAGAGGCCA UUUUAGGAAC CAAAGAAAGA**

1960 UUGUUAAGUG UUCAAUUGU GGCAAAGAAG **GGCACACAGC CAGAAAUUGC**

2010 AGGGCCCCUA GGAAAAAGGG CUGUUGGAAA UGUGGAAAGG AAGGACACCA

2060 AAUGAAAGAU UGUACUGAGA G

FIGURE 56

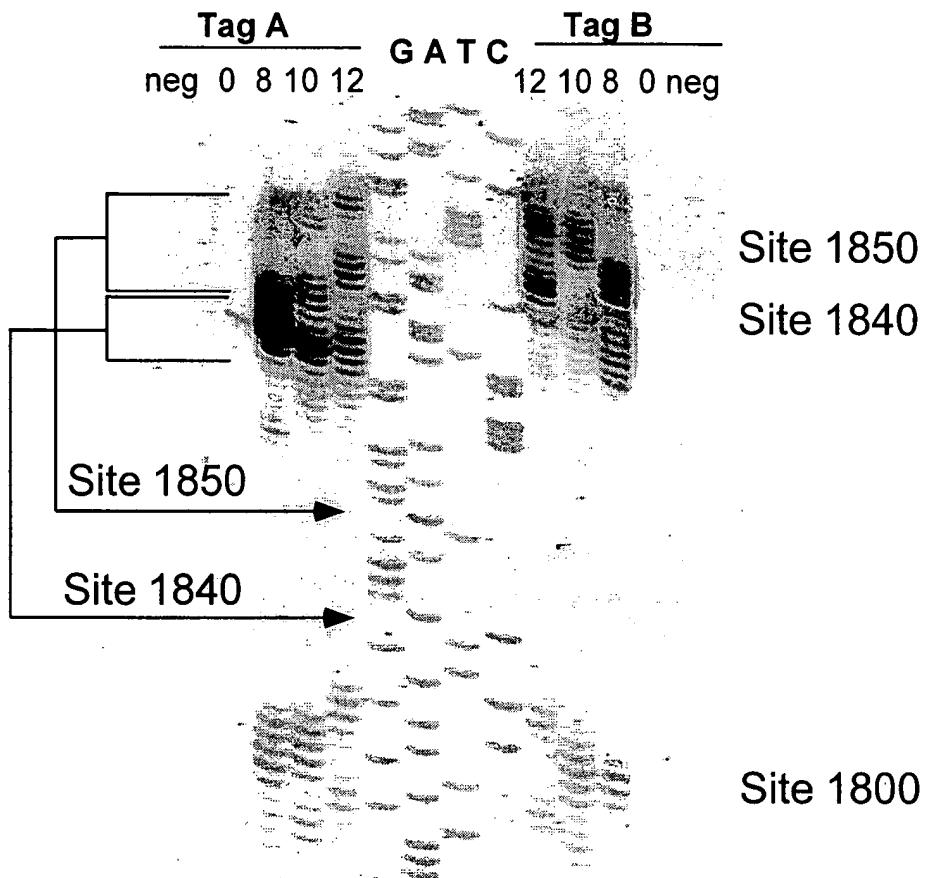


FIGURE 57

(SEQ ID NO:188)
 (SEQ ID NO:187)
 (SEQ ID NO:186)
 (SEQ ID NO:185)
 (SEQ ID NO:184)
 (SEQ ID NO:183)
 (SEQ ID NO:182)
 (SEQ ID NO:181)
 (SEQ ID NO:180)
 (SEQ ID NO:179)
 (SEQ ID NO:178)
 (SEQ ID NO:177)
 (SEQ ID NO:177) 5'-CAUGUCAGGGAGGUAGGAGGCCAUAAAGGCCAAGAGUUUGGCUGAAAGCAAUGAG-3'
 1 CAGTCCCTCATC
 2 AGTCCCTCATCC
 3 GTCCCTCATCCT
 4 TCCCTCATCCTC
 5 CCCTCATCCTCC
 6 CCTCATCCTCCT
 7 CTCATCCTCCTG
 8 TCATCCTCCTGG
 9 CATCCTCCTGGG
 10 ATCCTCCTGGGC
 11 TCCCTCCTGGGC
 12 CCTCCCTGGGCC
 13 CTCCCTGGGCCAA-*FL*-5',
 (SEQ ID NO:158)
 (SEQ ID NO:164)
 (SEQ ID NO:165)
 (SEQ ID NO:166)
 (SEQ ID NO:167)
 (SEQ ID NO:168)
 (SEQ ID NO:169)
 (SEQ ID NO:170)
 (SEQ ID NO:171)
 (SEQ ID NO:172)
 (SEQ ID NO:173)
 (SEQ ID NO:174)
 (SEQ ID NO:175)
 (SEQ ID NO:176)

FIGURE 58

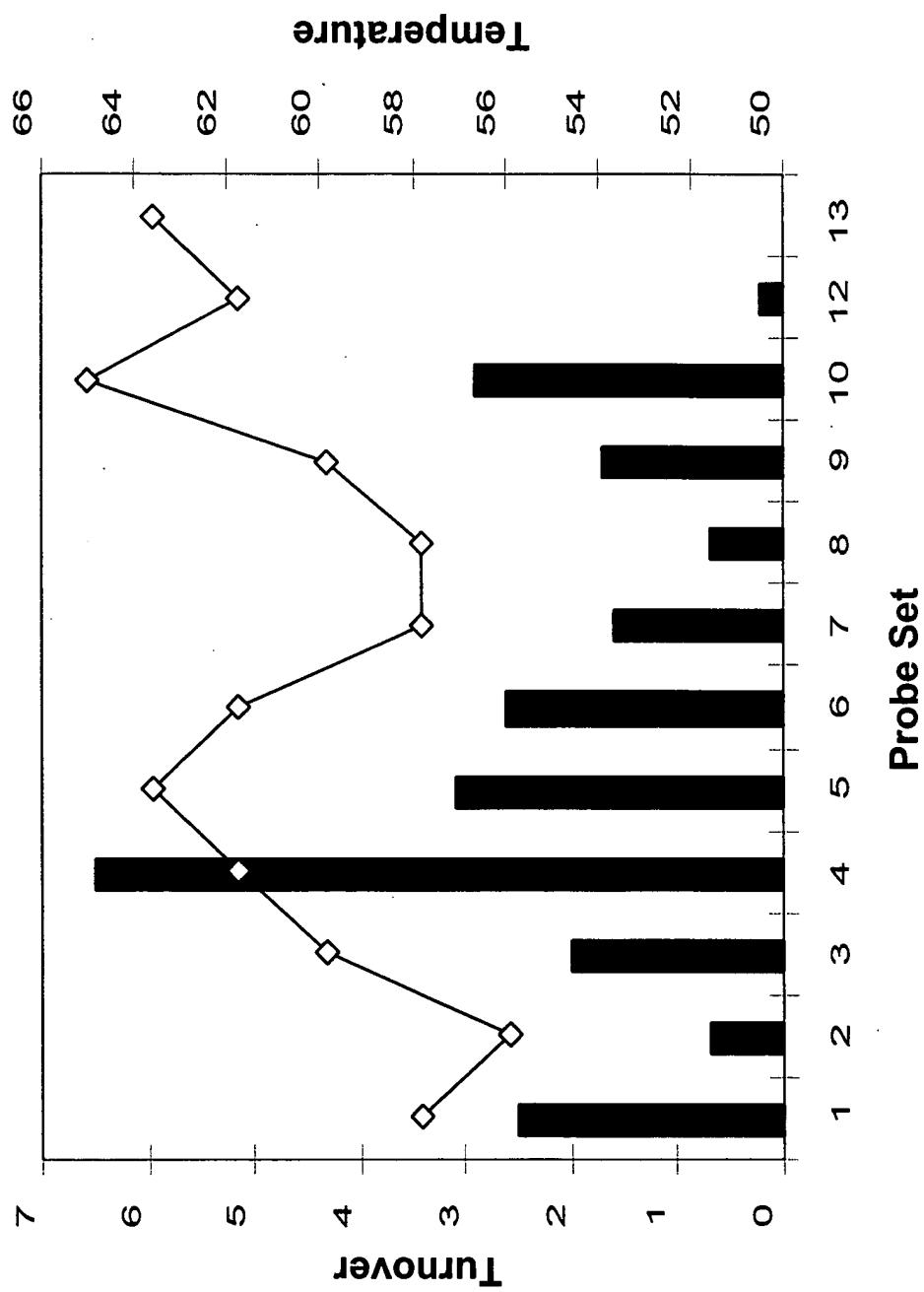


FIGURE 59

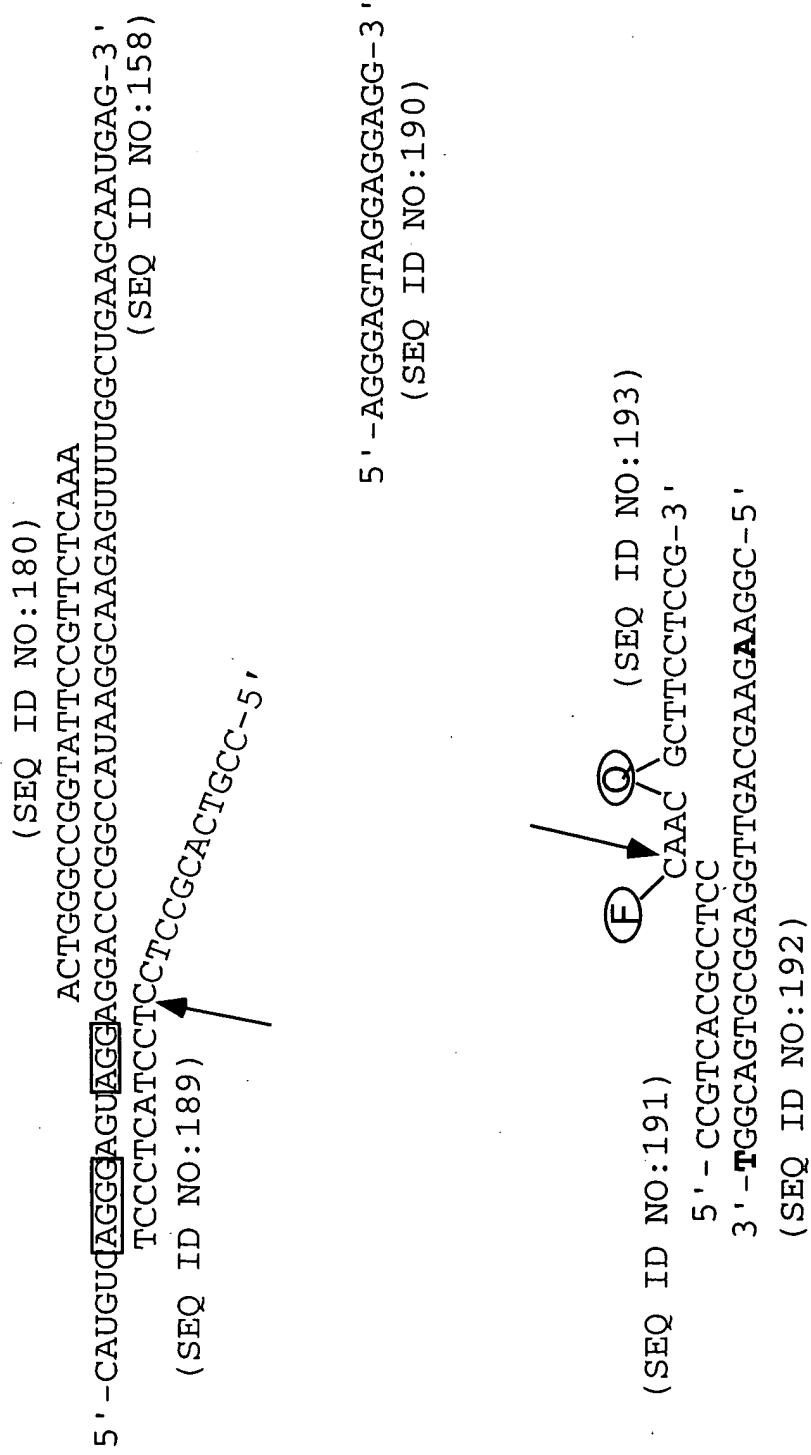


FIGURE 60

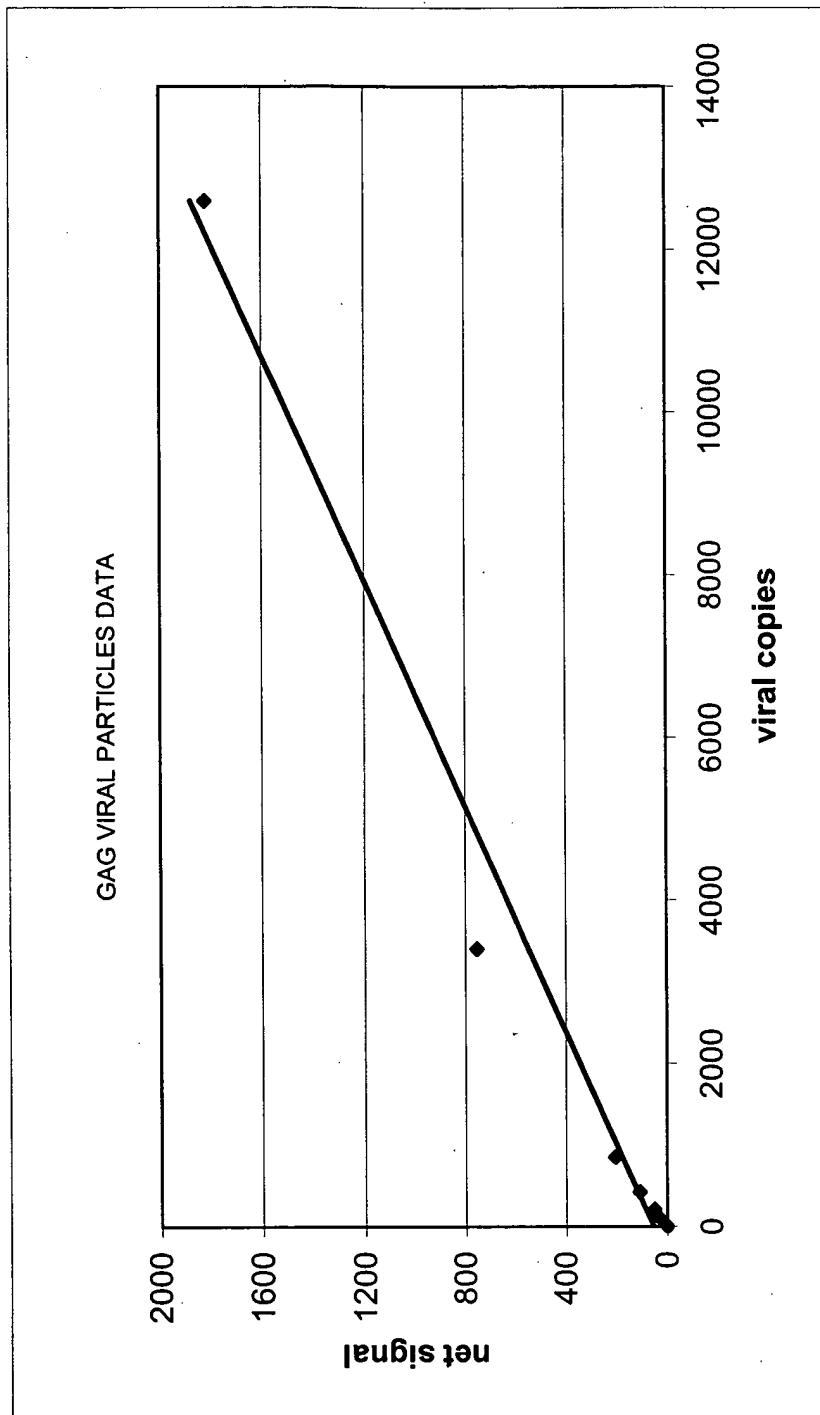


FIGURE 61A

SEQ ID NO:159

primer 1
3300 AGCUGGACUG UCAAUGACAU ACAGAA**GUUA** **GUGGGGAAAU** UG**AAUUGGGC**

3350 AAGUCAGAUU **UACCCAGGGA** UUA**AAGUAAG** GCAUUUAUGU AAACUCCUUA

3400 GAGGAACCAA AGCACUAACA GAAGUAAUAC CACUAACAGA AGAAGCAGAG

3450 CUAGAAC**UGG** CAGAAAACAG AGAGAUUCUA AAAGAAC**CAG** UACAUGGAGU

primer 2
3500 GUAAUUAUGAC **CCAUCAAAAG** ACUUAAUAGC AGAAAU**ACAG** **AAGCAGGGGC**

3550 **AAGGCCAAUG** GACAUAUCAA AUUUAU**CAAG** AGCCAUUUAA AAAUCUGAAA

3600 ACAGGAAAAU AUGCAAGAAU **GAGGGGUGCC** CACACUAAUG AUGUAAAACA

3650 AUUAAC**GAG** GCAGUGCAA AAAUAACCAC AGAAAGCAUA GUAAUAUGGG

primer 3
3700 GAAAGACUCC UAAAUUUA**AA** CUGCCCAUAC AAAAGGAAAC AUGGGAAACA

3750 UGGUGGACAG AGUAUUGGCA AGCCACCUGG AUUCCUGAGU GGGAGUUUGU

3800 UAAUACCCU CCCUUAGUGA AAUUA**UGGUA** CCAGUUAGAG AAAGAACCCA

3850 UAGU**AGGAGC** AGAAACCUUC UAUGUAGA**UG** **GGGCAGCUAA** **CAGG**GAGACU

primer 4
3900 AAAUUAGGAA AAGCAGGAUA UGUUACUAAU **AGAGGAAGAC** AAAAAGUUGU

FIGURE 61B

3950 CACCUAACU GACACAACAA AUCAGAAGAC UGAGUUACAA GCAAUUUAUC

4000 UAGCUUUGCA GGAAU~~C~~**GGA** UUAGAAGUAA ACAUAGUAAC AGACUCACAA

4050 UAUGCAAUAG GAAUCAUUC **A**~~G~~**CACAA**CCA GAUCAAAGUG AAUCAGAGUU

primer 5

4100 AGUCAAUCAA AUAAA~~GAGC~~ AGUAAAAGG AAAGGAAAAG GUCUAUC~~UGG~~

4150 **CAUGGGUACC** AGCACACAAA GGAUUGGAG GAAAUGAACA AGUAGAUAAA

4200 UUAGUCAGUG CUGGAAUCAG GAAAGUACUA UUUUUAGAUG GAAUAGAUAA

4250 **GGCCAAGAU** GAACAUGAGA AAUAUCACAG UAAUGGAGA GCAAUGGCUA

primer 6

4300 GUGAUUUUA CCUGCCACCU GUAGUAGCAA AAGAAAAGU **AGCCAGCUGU**

4350 GAUAAAUGUC AGCUAAAAGG AGAAGCCAUG CAUGGACAAG UAGACUGUAG

4400 UCCAGGAAUA UGGCAACUAG AUUGUACACA UUUAGAAGGA AAAGUUUAUCC

4450 UGGUAGCAGU UCAUGUAGCC AGUGGAUUA UAGAAGCAGA AGUUAUUCCA

primer 7

4500 GC**AGAAACAG** **GGCAG**GAAAC AGCAUUUU CUUUAAAUAGCAGGAAG

4550 **AUGGCCAGUA** AAAACAAUAC AUACUGACAA **UGGCAGCAAU** UUCACCGGUG

4600 CUACGGUUAG GGCGGCCUGU UGGUGGGCGG GAAUCA**AGCA** **GGAAUUUGGA**

FIGURE 61C

4650 AUUCCUACA AUCCCCAAAG UC**AAGGA**GUA GUAGAAUCUA UGAAUAAAGA

primer 8

4700 AUUAAAGAAA AUUAUAGGAC AGGUAAGAGA **UCAGG**CUGAA CAUCUUAAGA

4750 CAGCAGUACA AAUGGCAGUA UUCAUCCACA AUUUUAAAAG AAA**AGGG**GGG

4800 AUUGGGGGGU AC**AGUGCAGG** **GGA**AAGAAUA GUAGACAUAA UAGCAACAGA

4850 CAUACAAACU AAAGAAUUAC AAAAACAAAU UACAAAAAUU CAAAAUUUUC

primer 9

4900 GGGUUUAUUA CAGGGACAGC AGAAAUCAC UUUGG**AAGG** ACCAGCAAAG

4950 CUCCUCUGGA AAGGUG**AAGG** GGCAGUAGUA AUACAAGAUA AUAGUGACAU

5000 AAAAG**UAGUG** CCAAGAAGAA AAGCAAAGAU CAUUAGGGAU UAUGGAAAAC

5050 AGAUGGCAGG UGAUGAUUGU G

FIGURE 62

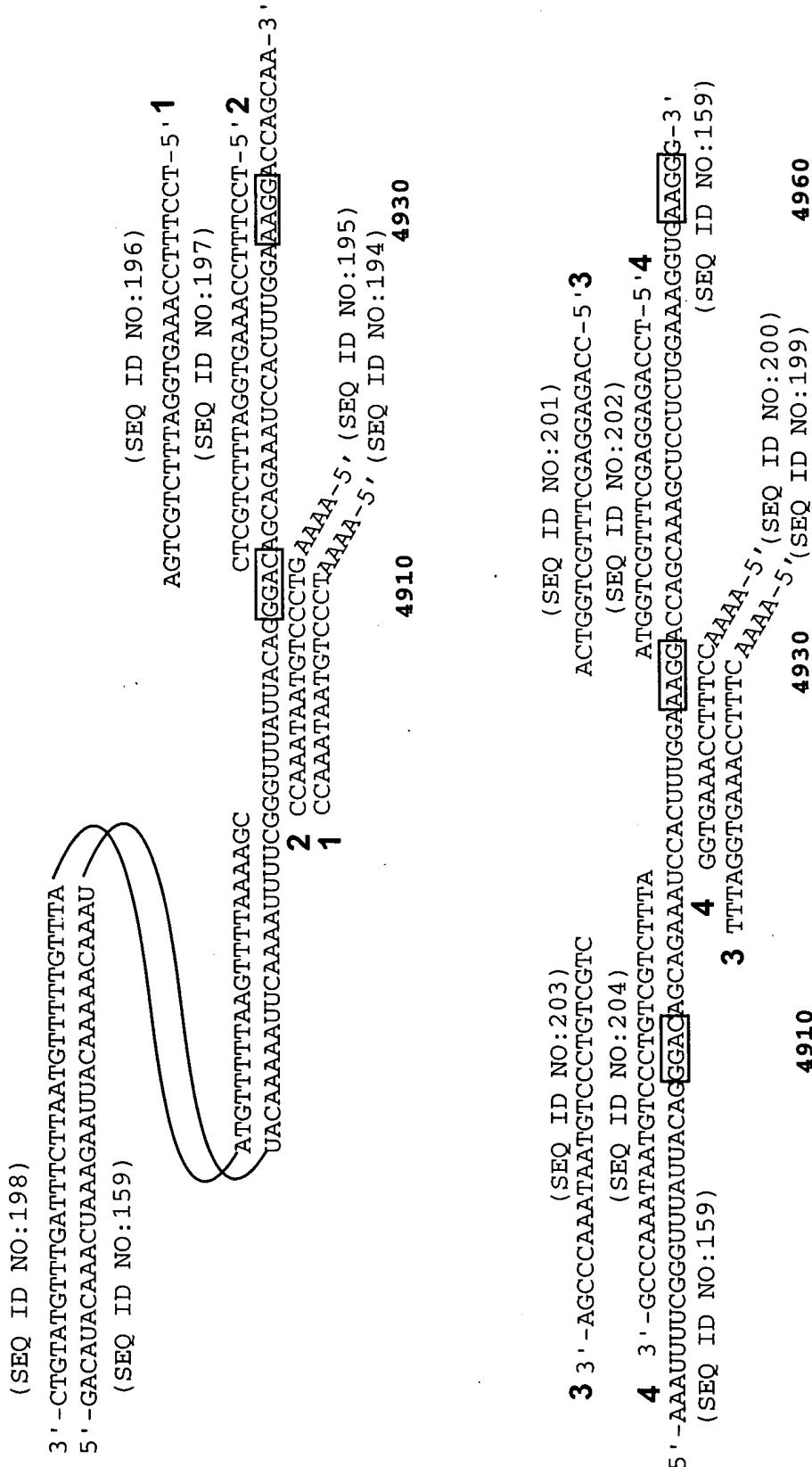


FIGURE 63

4930	5	3' - TCGAGGAGACCTTTCCAC (SEQ ID NO: 213)	ACCCGGTCACTCATTATGGTCTTATTACTGTATT-5' 5 (SEQ ID NO: 209)
	6	3' - CCTGGTCTGGTTTCGAGGAGAC 5' - GAAAGGAAACCAGCAAAGC (SEQ ID NO: 214)	ACCGTCACTCATTATGGTCTTATTACTGTATT-5' 6 ACGGTCACTCATTATGGTCTTATTACTGTATT-5' 6 (SEQ ID NO: 210)
	7	3' - TCGAGGAGACCTTTCCACT 5' - GAAAGGAAAGCUCUGGAAAGGUGA (SEQ ID NO: 215)	CTCATTATGGTCTTATTACTGTATT-5' 7 (SEQ ID NO: 211)
	8	3' - TCGAGGAGACCTTTCCACT 5' - GAAAGGAAAGCUCUGGAAAGGUGA (SEQ ID NO: 216)	ACATTATGGTCTTATTACTGTATT-5' 8 ACGGTCACTCATTATGGTCTTATTACTGTATT-5' 8 (SEQ ID NO: 212)
4930	7	3' - TCGAGGAGACCTTTCCACT 5' - GAAAGGAAAGCUCUGGAAAGGUGA (SEQ ID NO: 205)	TCCCCGGTCAAAAAA- 5 , (SEQ ID NO: 206) TCCCCGGTCAAAAAA- 5 , (SEQ ID NO: 207) 4960 (SEQ ID NO: 159) 5000

FIGURE 64

1

4790 4810

(SEQ ID NO: 224)

3' - TCCCCCTAACCCCCCATG
 5' - AAGAAAAGGGGAUTGGGGUACAGGGAAAGACAUAAUAGCAACAGACAUACAAACU-3'
 ATTTCCTTATCATCTGTATTATC GTGCTGTATGT-5'
 TCACGTCCCCAAAAA-
 (SEQ ID NO: 159)

25

(SEO ID NO: 2225)

3' -CTGTCGTATGTTACCGTCAATAAGTAGGT
 5' -AGACAGCAGUACAAUGGCAGUAUUCAUCCA

4790

(SEO ID NO: 222)

ACCTAACCCCCATGTCAC-5'
GGGGAUUGGGGUACAGUGCAGGGGAAAG-3'
(SEQ ID NO:159)

GTTAAATTTCTTTCCCTATATA-⁵, (SEQ ID NO: 220)
GTTAAATTTCTTTCCCTATATA-⁵, (SEQ ID NO: 218)

4790

(SEQ ID NO: 222)

5' - AAAAGGGGGAUGGGGGUACAGUCCCTAACCCCCCATGTAC-5'

(SEQ ID NO:223)

CATCATCTGTATTATCGTTGTCGTATGTTGATTIC
AAUAGUAGACAUAAAUAUAGCAACAGACAUACAAAGAA-3
TT₂, (SEQ ID NO:159)

4-5, (SEO ID NO: 219)

FIGURE 65

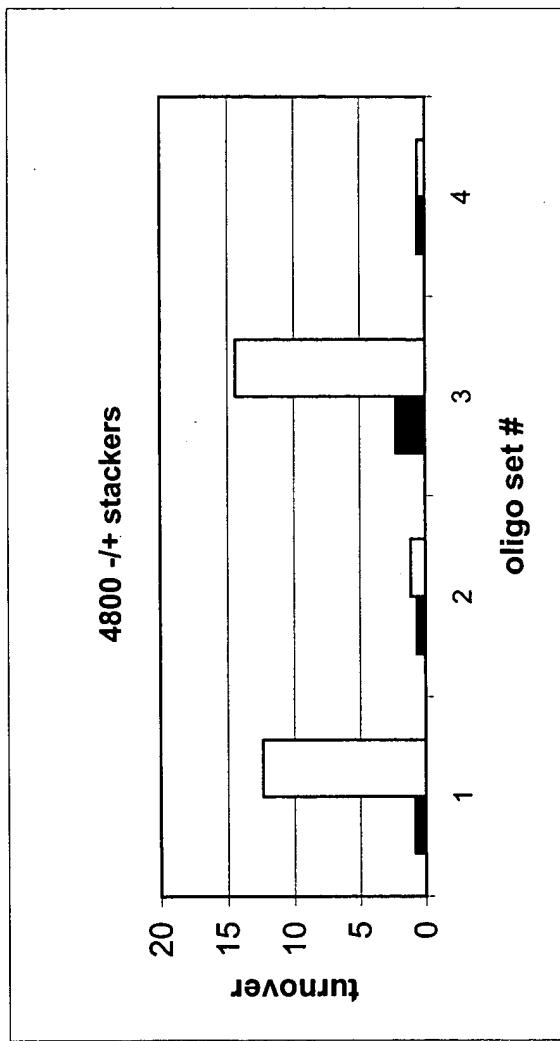


FIGURE 66

4790

(SEQ ID NO: 224)

3' - TCCCCCTAACCCCCCATG
5' - GAAAAGGGGGGAUUGGGGUAAAGGUAGACAUAAUAGCAACAUACUA-3'
(SEQ ID NO: 226)

TCACGTCCGCCCTCCGCACTGCC-5'

4810

(SEQ ID NO: 221)

ATTCTTATCATCTGTATTATCGTTGTCTGTATGT-5'
AGUGCAGGGGAAGAAUAGGUAGACAUAAUAGCAACAUACUA-3'
(SEQ ID NO: 159)

5' - AGTGCAGGGGGGGGG-3'
(SEQ ID NO: 227)

(SEQ ID NO: 191)

5' - CCGTCACGCC
3' - **T**GGCAGTGCGGAGGTGACGA**GAAAGGC**-5'
(SEQ ID NO: 192)

(SEQ ID NO: 193)

5' - CCGTCACGCC
3' - **T**GGCAGTGCGGAGGTGACGA**GAAAGGC**-5'
(SEQ ID NO: 192)

(SEQ ID NO: 191)

5' - CCGTCACGCC
3' - **T**GGCAGTGCGGAGGTGACGA**GAAAGGC**-5'
(SEQ ID NO: 192)

FIGURE 67

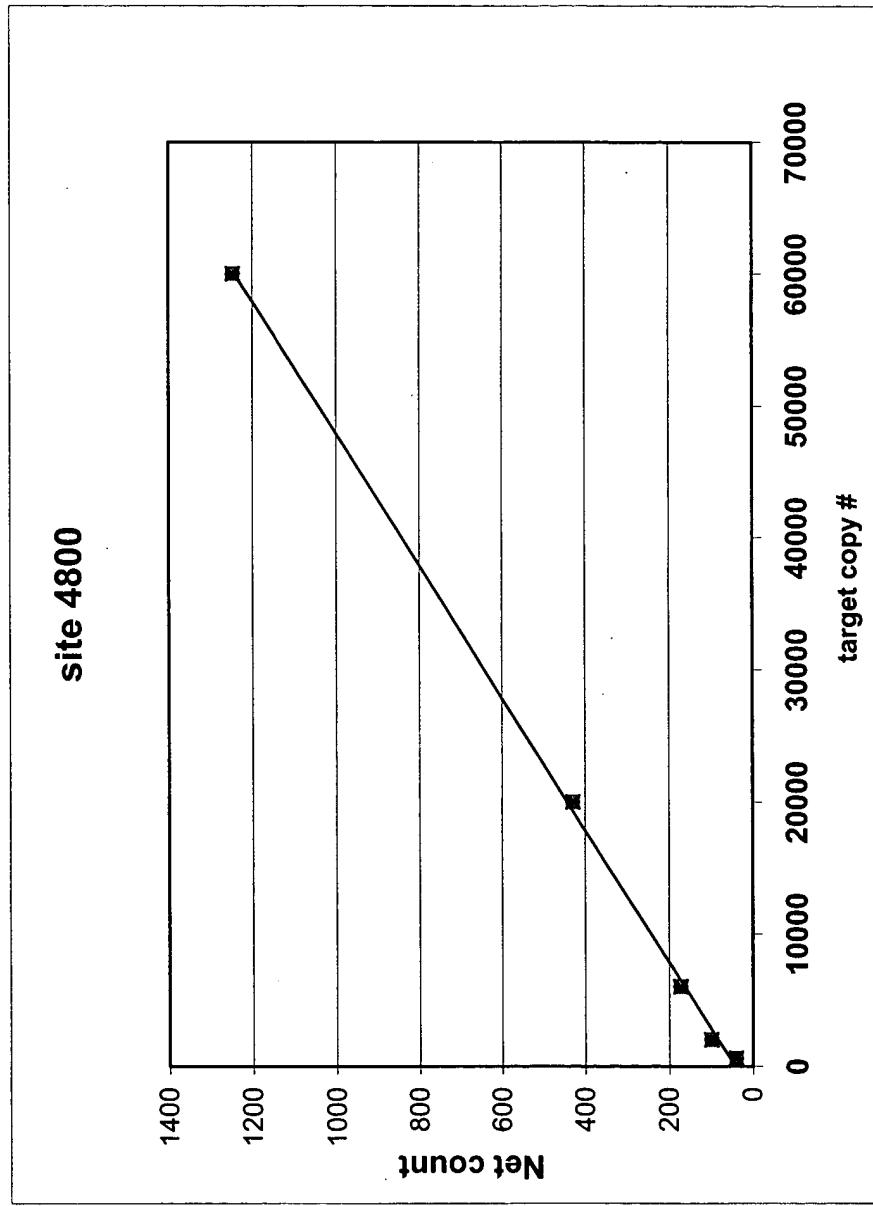


FIGURE 68

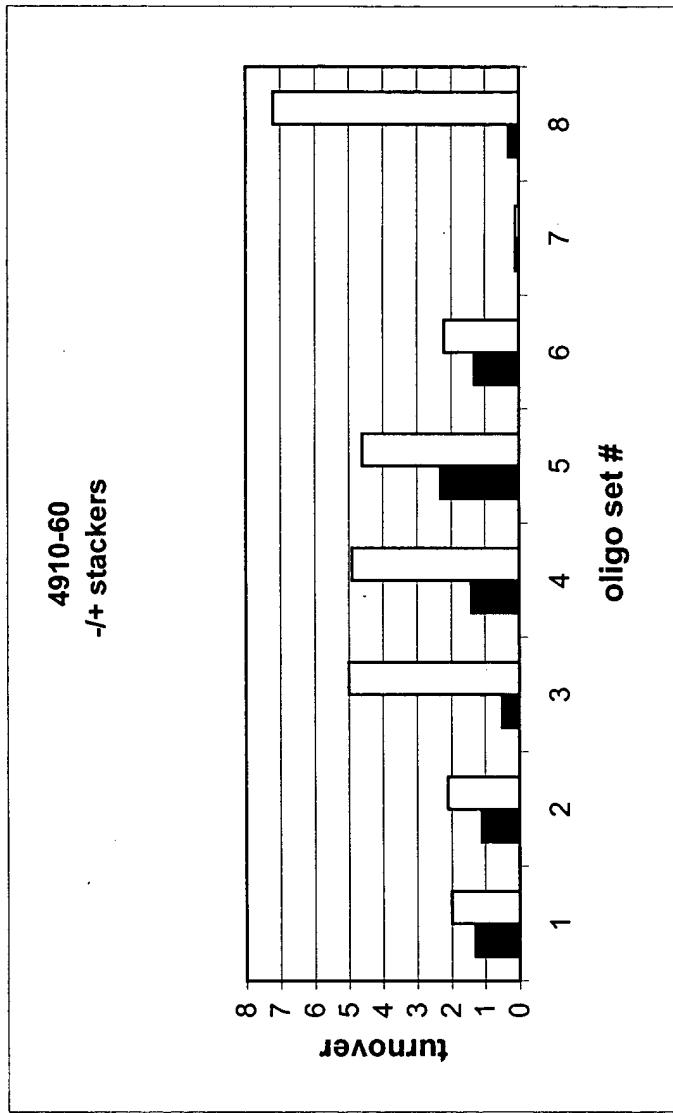


FIGURE 69

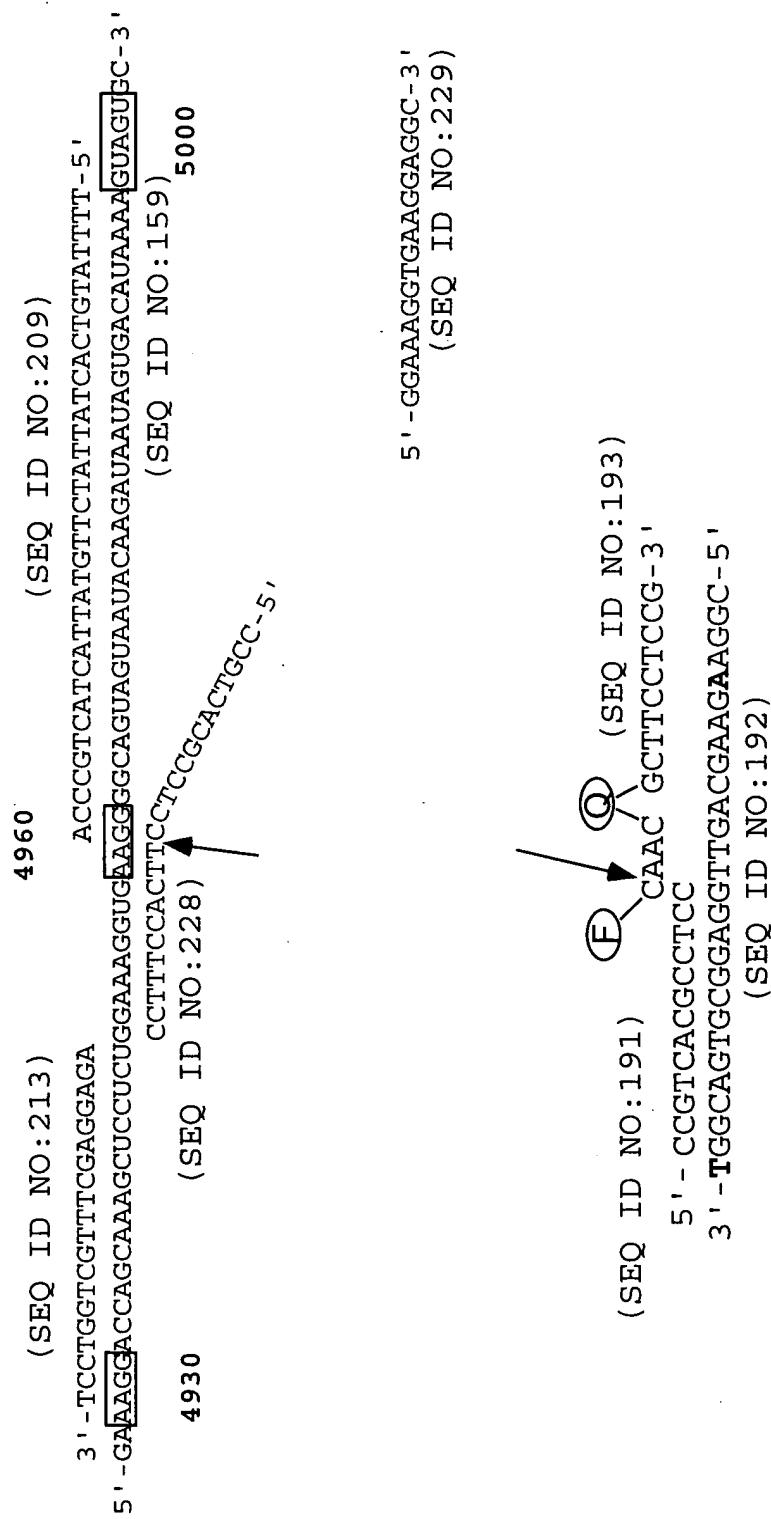


FIGURE 70

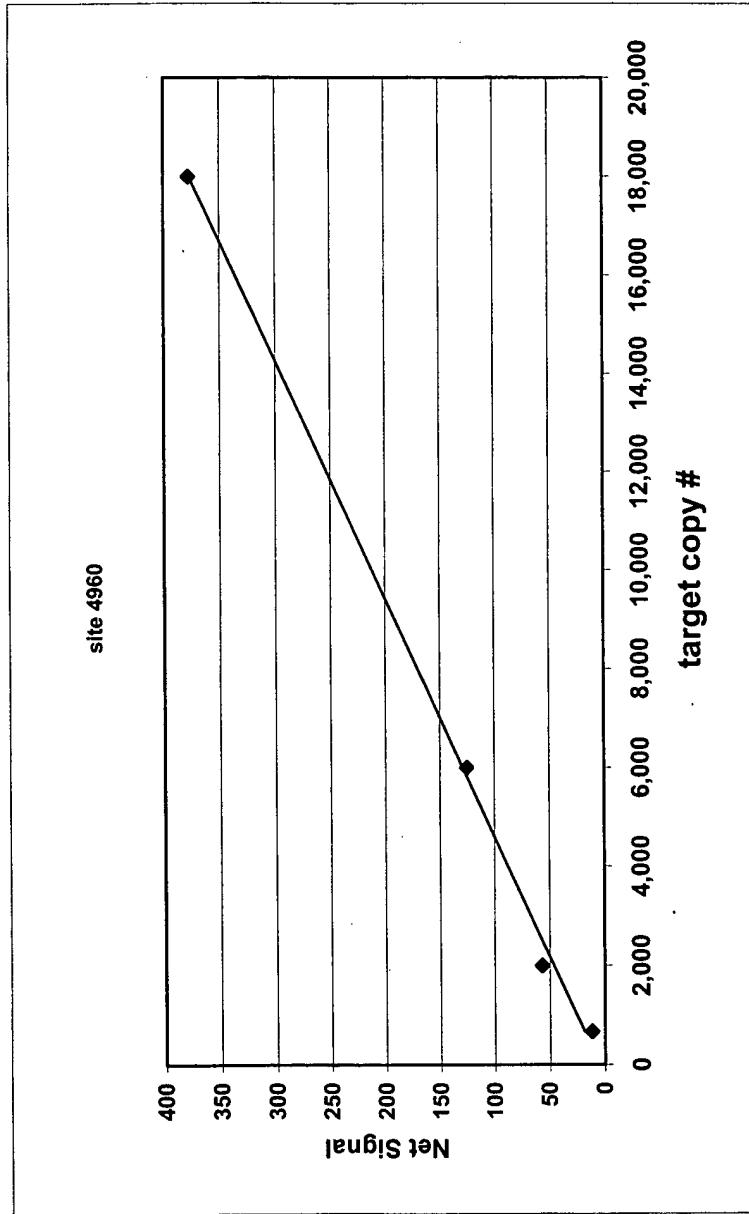


FIGURE 71

Human PSP94

383-31-1 5'-TET-CCTGCTTATCACAATGAA-3' (SEQ ID NO:230)
383-31-3 5'-TET-ACATGCACTTGCTACGAAAC-3' (SEQ ID NO:231)

SEQ ID NO:232

CCUGCUUAUCACAAUGAAUGUUCUCCUGG|GCAGCGUUG|UGAUCUUUGCACCUCGUGA
CUUUAUGCAAUGCAUCAUGCUAUUCAUACCUAAUGAGGGAGUCCAGGAGAUCAACCA
GGAAAUGCAUGGAUCUAAAGGAAACAAACACCCAAUAAACUCGG|AGUGG|CAGACUGAC
AACUGUG|AGACAUG|CAC|UJGCUACGAAAC|GAAAUUCAUGUU|GCACC|CUUGUUUCUAC
|ACCUGUGGGUUAUGACA|AAGACA|CUGCC|AAAGAAUC|UUCAAGAAGGGAGGA|CUGCAAGU
AUAUCG|UGGUGGAGAAGA|AGGACC|CAAAAAAGACCUGUUCUGUCAGUGAAUGGAUAUC
UAAUGUGCUUCUAGUAGGCACAGGGCUCCAGGCCAUUCUCCUCUGGCCUCUA
AUAGUCAAUGAUUGUGUAGCCAUGCCUAUCAGUAAAAGAUUUUUG

FIGURE 72

Human ubiquitin:

520-77-1 5'-TET-CCGCCACCAAAATGC-3' (SEQ ID NO:233)

520-59-2 5'-TET-GCTGGAAGATGGACG-3' (SEQ ID NO:234)

SEQ ID NO:235

CCGCCACCAAAUUGCAGAUUUUCGUGAAAACCUUACGGGGAAGACCAUCACCCUCGAG
GUUGAACCCUCGGAUACGAUAGAAAAUGUAAAGGCCAAGAUCCAGGAUAGGAAGGAAU
UCCUCCUGACAGCAGAGACUGAUCUUUGCUGGCAAGCAGCUGGAAGAUGGACGUACUUUG
UCUGACUACAAUAUCAAAAGGAGUCUACUCUUCAUCUUGUGUUGAGACUUCGUGGUGG
UGCUAAGAAAAGGAAGAAGAAGUCUUACACCACUCCAAGAAGAAUAAGCACAAGAGAAA
GAAGGUUAGCUGGCUGGUCCUGAAAUUAAGGUGGAUGAGAAUGGCAAAAUAGUC
GCCUUCGUCGAGAGUGGCCUUCUGAUGAAUGUGGUGCUGGGUGUUUAUGGCAAGUCACU
UUGACAGACAUUAUUGUGGCAAUAUGUUGUCUGA

FIGURE 73

HCV-1a 5' -UTR:

898-28-01 5'-TET-GGGACACTCCACCATGAATCACTC-3' (SEQ ID NO:236)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGC GG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTGGGCGTCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACC GGTCCTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:240

GGGACACUCCACCAUGAAUCACUCCCCUGUGAGGAACUACUGUCUUACGCAGAAAGCGU
CUAGCCAUGGCCGUUAGUAUGAGUGUGCGUGCCAGGACCCCCCCUCCGGGAGAG
CCAUAGUGGUCUGCGAACCGGUGAGUACACCGGAAUUGCAGGACGACCGGGGUCCUUUC
UUGGAUAAACCCGCUCAAUGCCUGGAGAUUGGGGUGCCCGCAAGACUGCUAGCC
AGUAGUGUUGGGUCGCGAAGGCUUGGUGGC
CCGGGAGGUCGUAGACCGUGAGAG

FIGURE 74

HCV-1b 5'-UTR:

898-28-02 5'-TET-GGGACACTCCACCATAGATCACTC-3' (SEQ ID NO:241)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGC GG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACC GGTCCTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:242

GGGACACUCCACCAUAGAUCACUCCCCUGUGAGGAACUACUGCUUCACGCAGAAAGCGU
CUAGCCAUGGCCUUAGUAUGAGUGUGUCGUGCAGCCUCCAGGACCCCCCCCUCCCCGGGAGAG
CCAUAGUGGUUCUGC GGAA CCGGUGAGUACACCGGAAUUGC CAGGACGACCGGGUCCUUUC
UUGGAUCAACCCGCUCAAUGCCUGGAGAUUUGGGCGUGCCCCCGCGAGACUGCUAGCCG
AGUAGUGUUGGGUCGC GAAAGGCCUUGUGGUACUGC CUGAUAGGGUGCUUGC GAGUGCC
CCGGGAGGUCUGUAGACCGUGCACCAUGAG

FIGURE 75

HCV 2a/c 5'-UTR:

898-28-01 5'-TET-GGGACACTCCACCATGAATCACTC-3' (SEQ ID NO:236)

898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)

898-35-02 5'-TET-ATTGGGCGTGCCCCGC-3' (SEQ ID NO:238)

898-35-03 5'-TET-GACCGGGTCCTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:243

GGGACACUCCACCAUGAAUCACUCCCCUGUGAGGAACUACUGCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUACAGCCUCCAGG~~CCCCCC~~UC~~CCG~~GGAGAG
CCAUAGUGGUCUGCGAACCGGUGAGUACACCGGAAUUGC~~GGGA~~AGACUGGGUCCUUUC
UUGGAUAAACCCACUCUAUGCCC~~GG~~CAUUUGGGCGUGCCCCGCAAGACUGCUAGCCGA
GUAGCGUUGGGUUGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCCCC
GGGAGGUCUGUAGACCGU~~G~~CACCAUGAG

FIGURE 76

HCV 3a 5'-UTR:

898-28-03 5'-TET-GGGACACTCCACCATGGATCACTC-3' (SEQ ID NO:244)
898-35-01 5'-TET-CGGGAGAGGCCATAGTGGTCTGC GG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACC GGTCCTTCTT GGA-3' (SEQ ID NO:239)

SEQ ID NO:245

GGGACACUCCACCAUGGAUCACUCCCCUGUGAGGAACUUUCUGCUUCAGCGGAAAGCGC
CUAGCCAUGGCGUUAGUACGAGUGUCGUGCAGCCUCCAGGCCCCCCCCUC~~CCG~~GGAGAG
CCAUAGUGGUUCUGCGGAACCGGUGAGUACACCGGAAUCGCUGGGGUGACCGGGUCCUUUC
UUGGAA~~CAACCC~~GCUCAAUACCCAGAAA~~UU~~UGGGCGUG~~CCCC~~CGCGAGAUCAC~~UAGCCG~~
AGUAGUGU~~UGG~~GU~~CG~~GAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCAGUGCC
CCGGGAGGUUCGUAGACCGU~~GG~~CACCAUGAG

FIGURE 77A

Human Antigen CD36 mRNA Oligonucleotides

726-38-01	5'-ACAAGGGAAGAGAGATGAGGAACCAG-3'	(SEQ ID NO:246)
666-33-01	5'-TTTGCCTTCTCATCACCAATGG-3'	(SEQ ID NO:247)
937-03-01	5'-TET- aagggaagagagatgag-3'	(SEQ ID NO:248)
937-03-02	5'-TET-aggagttgcaagaaac-3'	(SEQ ID NO:249)
937-03-03	5'-TET-ggtgctgtcctgg-3'	(SEQ ID NO:250)
937-03-04	5'-TET-cagtttggatcttgatg-3'	(SEQ ID NO:251)
937-03-05	5'-TET-aggacgctgagga-3'	(SEQ ID NO:252)
937-03-06	5'-TET-aacaagtcaaaatcttctatg-3'	(SEQ ID NO:253)
937-03-07	5'-TET-caataactgcagatggag-3'	(SEQ ID NO:254)
937-03-08	5'-TET-aagccaggtattgca-3'	(SEQ ID NO:255)
937-03-09	5'-TET-ctattgttctgcacaga-3'	(SEQ ID NO:256)
937-03-10	5'-TET-aaatgaagaagaacatagga-3'	(SEQ ID NO:257)
937-03-11	5'-TET-ggtcaagccatcaga-3'	(SEQ ID NO:258)

FIGURE 77B

Human Antigen CD36 mRNA (SEQ ID NO:259)

FIGURE 78

Human Ribosomal Protein L5 mRNA

761-47-01	5'-ATGGGGTTTGTAAAGTTG-3'	(SEQ ID NO:260)
761-47-02	5'-GCTGGGTTAGCTCTCAGCAGCCGC-3'	(SEQ ID NO:261)
937-05-01	5'-TET- atggggtttgttaaagt-3'	(SEQ ID NO:262)
937-05-02	5'-TET- gaagacgacgagagg-3'	(SEQ ID NO:263)
937-05-03	5'-TET- ggatgatagttcgtgt-3'	(SEQ ID NO:264)
937-05-04	5'-TET- gctgcagcatattgt-3'	(SEQ ID NO:265)
937-05-05	5'-TET- ctgctattggatgca-3'	(SEQ ID NO:266)
937-05-06	5'-TET- gcagaagtacatcgga-3'	(SEQ ID NO:267)
937-05-07	5'-TET- gacatgatggaggaga-3'	(SEQ ID NO:268)
937-05-08	5'-TET- agaagaaggatcg-3'	(SEQ ID NO:269)

SEQ ID NO:270

AUGGGGUUUGUAAAAGUUGUUAAAGAAUAAGGCCUACUUUAAGAGAUACCAAGUGAAUU
UAGAAGACGACGAGAGGGUAAAACUGAUUAAAUGCUCGGAAACGCUUGGUGAUACAAG
AUAAAAAAUAAUACAAACACACCCAAAUACAGGAUGAUAGUUCGUGUGACAAACAGAGAU
AUCAUUUGUCAGAUUGCUU AUGCCCGUAUAGAGGGGAUAUGAUAGUCUGCGCACGUUA
UGCACACGAACUGCCAAAUAUGGUGUGAAGGUUGGCCGACAAUUAUGCUGCAGCAU
AUUGUACUGGCCUGCUGCUGGCCCGCAGGCUUCUCAAUAGGUUUGGCAUGGACAAGAUC
UAUGAAGGCCAAGUGGAGGUGACUGGUGAUGAAUACAAUGUGGAAAGCAUUGAUGGUCA
CCAGGUGCCUUCACCUGCUAUUJGGAUGCAGGCCJGCCAGAACUACCACUGGCAA
AGUUJUUGGUGCCCUGAAGGGAGCUGUGGAUGGAGGUUGUCUAUCCCUCACAGUACCA
AACGAUUCCCGGUUAUGAUUCUGAAAGCAAGGAAUUUAUGCAGAAGUACAUGGAAG
CACAUAUGGCCCAGAAUGUUGCAGAUUACAUGCGCUACUUAAUGGAAGAAGAUGAAGA
UGCUUACAAGAACAGUUCUCUCAAUACAUAAAGAACAGCGUAACUCCAGACAUGAUGG
AGGAGAUGUAUAAGAAAGCUCAUGCUGCUUACGAGAGAAUCCAGUCUAUGAAAAGAAG
CCCCAGAAAGAAGUAAAAAGAAGAGGUGGAACCGUCCCAAAUGUCCCUUGCUCAGAA
GAAGGAUCGGGGUAGCUAAAAGAAGGCAAGCUUCCUCAGAGCUCAGGAGCGGGCUGCUG
AGAGCUAAACCCAGC

FIGURE 79A

Mouse Scavenger Receptor Class B Type I mRNA Oligonucleotides

726-39-01	5'-GCTCAAGAACATGTCCGCATAGACCCG-3'	(SEQ ID NO:271)
666-34-01	5'-CTGGTCCCTGAGTTGTTTTGC-3'	(SEQ ID NO:272)
937-01-01	5'-TET- GCTCAAGAACATGTCCG-3'	(SEQ ID NO:273)
937-01-02	5'-TET- gggatgtggaaggag-3'	(SEQ ID NO:274)
937-01-03	5'-TET- ggaccctatgtctacag-3'	(SEQ ID NO:275)
937-01-04	5'-TET- acatcttggtcctgg-3'	(SEQ ID NO:276)
937-01-05	5'-TET- tctcaaacacgtacctc-3'	(SEQ ID NO:277)
937-01-06	5'-TET- cggactcagcaaga-3'	(SEQ ID NO:278)
937-01-07	5'-TET- caagggtgttgaagg-3'	(SEQ ID NO:279)
937-01-08	5'-TET- ctctgtttctctccca-3'	(SEQ ID NO:280)
937-01-09	5'-TET- gtgaagatgcagctg-3'	(SEQ ID NO:281)
937-01-10	5'-TET- agctggtgctgatg-3'	(SEQ ID NO:282)
937-01-11	5'-TET- caggcctactctgag-3'	(SEQ ID NO:283)
937-01-12	5'-TET- ggactctctcagcg-3'	(SEQ ID NO:284)

FIGURE 79B

Mouse Scavenger Receptor Class B Type I mRNA (SEQ ID NO:285)

GCUCAGAAUGUCCGCAUAGA[CCC]GAGCAGCCUGUCCUUCGGGAUGUGGAAGGAGAUCC
CCGUCCCCUUUCUACUUGUCUGUCUACUUUCUGAAGUGGUCAACCCAAAC[GAG]GUCCUC
AACGGCCAGAAGCCAGUAGU[CGGG]AGCGUGGACCCUAUGUCUAC[AGG]GAGUUCAGACA
AAAGGUCAACACCUUCAAUGACAACGACACC[GUGUCCUUCGUGGAGAA][CCGCAGC]C
UCCAUUUCCAGCCUGACAAGUCGCAUGGCUCAGAGAGUGACUACAUUGUACUGCCUAACA
UCUUGGUCCUGGGGGCUCGAUUAUG[AUGGAG]AGCAAGCCUGUGAGCCUGAAGCUGAUG
AUGACCUUGGCCUGGUACCCAUGGGCCAGCGUGCUUUUAUG[AACC]GCACAGUUGGUGA
GAUCCUGUGGGCUAUGACGAUCCUUCGUGCAUUUCUCAACACGUACCUCAGACAU
GCUUCCCAUAAGGGAAAUUUGCCUGUUUGUUGGAUGAACACUCGAAUUC[UGGG]
UCUUCACUGUCUUC[ACGG]GCUCCAGAAUUUC[AGCA]GGAUCCAUCUGGUGGACAAUUGG
AACGGACUCAGCAAGAUCGAUUAU[U GGCAUUCAGAGCA]GUGUAACAUGAUCAA[U GG]GAC
U[UCCGG]GAGAUG[UGGG]ACCCUUC[UGACACC]CGA[AUCCUC]GCUGGAAUUCUUCAGCC
[CGG]GGCAUGCAGGUCCAUGAAGCUGACCUACAACGAAUCAAGGGUGUUUGAAGGCAU
CCCACGUACGCUUC[ACGGCC]CCCGAUACUCUGUUUGCCAACGGGUCCGUCUACCCACC
CAACGAAGGCUUCUGCCCAUGCCGAGAGUCUGGCAUUCAGAAUGUCAGCACCUGCAGGU
UGGUGCGCCUCUGUUUCUCUCCACCCCCACUUUUA[CACGCCGAC]CCUGUGUUGUCAG
AAGCUGUUUCUUGGUCUGAACCCUAACCCAAAGGAGCAUUCUUGUUCUAGACAUCCA[U
CGGU]CACUGGGAUCCCCAUGAACUGUUUCUGUGAAGAU[GCA]GC[UGA]GCCCUACAUCA
AUCUGUCAAGGGCAUCGGCAAACAGGGAAAGAUCGAGCCAGUUCUGCCGUUGCUGUG
GUUCGAACAGAGCGGAGCAAUGGGUGGCAAGCCCCUGAGCAGUUCUACACGCAGCUGGU
GCUGAUGCCCCAGGUUCUUCACUACGCGCAGUAUGUGCUGCUGGGCUUGGAGGCCUCCU
GUUGCUGGUGCCCAUCAUCUGCCAACUGCGC[AGCCAGGA]GAA AUGCUUUUUGUUUUGGA
GUGGUAGUAAAAGGGCUCCAGGAUAAGGAGGCCAUCAGGCCUACUCUGAGUCCUGAAGACA
CUAUAG[CCCC]CAAACCUGAUAGCUUGGUCAAGGAGCCACCGCCACCCAGUCCUACACCCCG
CUUCUUGAGGACUCUCAGCGGACAGCCCACCAUGGCCAUGGCCUGAGCCCCAGAUGU
CACACCUGUCCGCACGCACGGCACAUUGGAUGGCCACGCAUGUGCAAAAACAACUCAGGG
CCAG

FIGURE 80A

Rat CX3CR1 Accession No. U04808 Oligonucleotides

761-57-01	5'-taatacgactcactatagggacggaagtccaaaggcatcactg-3'	(SEQ ID NO:286)
761-57-03	5'-gcaggtacctggtccgta-3'	(SEQ ID NO:287)
781-65-01	5'-TET-ggaagtccaagagca-3'	(SEQ ID NO:288)
781-65-02	5'-TET-aatggcttcttggg-3'	(SEQ ID NO:289)
781-65-03	5'-TET-ggcgtcgccc-3'	(SEQ ID NO:290)
781-65-04	5'-TET-tacttccgcatcgtc-3'	(SEQ ID NO:291)
781-65-05	5'-TET-cttcttccttagtttg-3'	(SEQ ID NO:292)
781-65-06	5'-TET-tgcctggccgt-3'	(SEQ ID NO:293)
781-65-07	5'-TET-gactctactaagaacc-3'	(SEQ ID NO:294)
781-73-01	5'-TET-ccatcttagtggcgt-3'	(SEQ ID NO:295)
781-73-02	5'-TET-caacaagtgcctgg-3'	(SEQ ID NO:296)
781-85-01	5'-TET-aacacggcgtcac-3'	(SEQ ID NO:297)
781-85-02	5'-TET-tgattaccccggagg-3'	(SEQ ID NO:298)
781-85-03	5'-TET-acgctgtttcctg-3'	(SEQ ID NO:299)
781-85-04	5'-TET-tgagacacacctgtacaa-3'	(SEQ ID NO:300)
781-85-05	5'-TET-gacggagacagtgg-3'	(SEQ ID NO:301)
781-85-06	5'-TET-caagcgagggagag-3'	(SEQ ID NO:302)

FIGURE 80B

Rat CX3CR1 Accession No. U04808 (SEQ ID NO:303)

FIGURE 81A

Human Interleukin-1 beta (IL-1 β) Oligonucleotides

720-82-01 5'-

gtaatttaatacgactcactatagggaagggtgcagtttgccaggagtgctaaag-3'
(SEQ ID NO:304)

562-15-01 5'-ctgattgaaatttatctaataaaacatcat-3'

(SEQ ID NO:305)

781-50-01 5'-TET-acttccaagctggc-3' (SEQ ID NO:306)

781-50-02 5'-TET-gagagtggaccacac-3' (SEQ ID NO:307)

781-50-03 5'-TET-gaatcagtgaagatgcc-3' (SEQ ID NO:308)

781-50-04 5'-TET-cattgtaccatgaaatatcc-3' (SEQ ID NO:309)

781-50-05 5'-TET-gaacttaattcaggaattg-3' (SEQ ID NO:310)

781-50-06 5'-TET-cccttagtctgctagc-3' (SEQ ID NO:311)

781-50-07 5'-TET-ttcaagtgttaacttattaacc-3' (SEQ ID NO:312)

781-72-01 5'-TET-aagctggccgtg-3' (SEQ ID NO:313)

781-72-02 5'-TET-tgcagtttgccaaag-3' (SEQ ID NO:314)

FIGURE 81B

Human Interleukin-1 beta (IL-1 β) (GenBank Accession # M15330) (SEQ ID NO:315)

GGCAGAAGUACCUGAGCUCGCCAGUGAAAUGAUGGCUUAUUACAGUGGCAAUGAGGAAUG
ACUUGUUUUUGAAGCUGAUGGCCCUAAACAGAUGAAGUGCUCUCCAGGACCUGGAC
CUCUGCCCUCUGGAUGGGCAUCCAGCUACGAAUCUCCGACCACCACUACAGCAAGGG
CUUCAGGCAGGCCGCGUCAGUUGUUGUGGCCAUGGACAAGCUGAGGAAGAUGCUGGUUC
CCUGCCCACAGACCUUCCAGGAGAAUGACUGAGCACCUUCCUUCAUCUUUGAA
GAAGAACCUAUCUUCUUCGACACAUGGGAUAACGAGGCUUAUGUGCACGAUGCACCUGU
ACGAUCACUGAACUGCACGCUCCGGACUCACAGCAAAAAGCUUGGUGAUGUCUGGUC
CAUAUGAACUGAAAGCUCUCCACCUCCAGGGACAGGAUAUGGAGCAACAAGUGGUGUUC
UCCAUGGUCCUUUGUACAAGGAGAAAGUAAUGACAAAACCUGUGGCCUUGGGCCUC
AAGGAAAAGAAUCUGUACCUGUCCUGCGUGUUGAAAGAUGAUAGCCCACCUACAGCU
GGAGAGUGUAGAUCCCAAAAUACCCAAAGAAGAAGAUGGAAAGCGAUUUGCUUCAA
CAAGAUAGAAAUCAAUAACAAGCUGGAAUUUGAGUCUGCCCAGUUCCCAACUGGUACA
UCAGCACCUCUCAAGCAGAAACAUGCCCCGUCCUGGGAGGGACCAAGGCGGCCAG
GAUUAACUGACUUCACCAUGCAUUUGUGCUUCCUAAAGAGAGAGCUGUACCCAGAGAG
UCCUGUGCUGAAUGUGGACUCAUCCCUAGGGCUGGCAGAAAGGGACAGAAAGGUUUU
UGAGUACGGCUAUAGCCUGGACUUUCCUGUUGUCUACACCAAUGCCACUCCUGCCU
AGGGUAGUGCUAAGAGGAUCUCCUGGUCAUAGCCAGGACAGUCAGCUCUCCUUU
CAGGCCAAUCCCCAGCCCCUUUJGUUGAGCCAGGCCUCCUCACCUCUCCUACUAA
AGCCCGCCUGACAGAAACCACGGCCACAUUUGGUUCAAGAAACCCUCUGUCAUUCGU
CCCACAUUCUGAUGAGCAACCGUUCCCUAUUUAUUAUUAUUUUGUUUGUUUGUUUUA
UUCAUUGGUUUAAUUAUCAAAGGGGCAAGAAGUAGCAGUGUCUUAAAAGAGCCU
GUUUUUAUAGCUAUGGAAUUCAAUUCAUUUGGACUGGUGUGCUCUUUAAAUAUCAAGU
CCUUUUAAGACUGAAAAAUAUAAGCUCAGAUUAUUAAAUGGGAAUUUUUAUAA
AUGAGCAAAUAUCAUACUGUUCA

FIGURE 82A

Human Interferon gamma Oligonucleotides

448-59-01 5'-TET-GCATCGTTTGCGGTTCTCTT (SEQ ID NO:316)

448-59-02 5'-TET-ACTTAAAGATGACCAGAGC (SEQ ID NO:317)

448-79-01 CACATTGTTCTGATCATCTG (SEQ ID NO:318)

448-79-02 CGGTAACTGACTTGAATGTC (SEQ ID NO:319)

448-79-03 TAGTAACTGGATAAGTATCAC (SEQ ID NO:320)

448-79-04 GACATTCAAGTCAGTTACCG (SEQ ID NO:321)

498-20-01 AATTTAACGACTCACTATACACATTGTTCTGATCATCTG
(SEQ ID NO:322)

498-20-02 AATTTAACGACTCACTATACGGTAACTGACTTGAATGTC
(SEQ ID NO:323)

498-20-03 5'-TET-CACATTGTTCTGATCATCTG (SEQ ID NO:324)

498-20-04 5'-TET-CGGTAACTGACTTGAATGTC (SEQ ID NO:325)

498-40-01 5'-
AGTAATTACGACTCACTATAGGGACACATTGTTCTGATCATCTGAAGA
(SEQ ID NO:326)

498-40-02 5'-
AGTAATTACGACTCACTATAGGGACGGTAACTGACTTGAATGTCCAAC
(SEQ ID NO:327)

498-84-01 5'-TET-CATTCAGATGTAGCG (SEQ ID NO:328)

498-84-02 5'-TET-GACTCATCAATCAA (SEQ ID NO:329)

498-84-03 5'-TET-GATTACAAGGCTTTA (SEQ ID NO:330)

FIGURE 82B

Human Interferon gamma (SEQ ID NO:141)

CACAUUGUUCUGAUCAUCUGAAGAUCAGCUAUAGAAGAGAAAGAUCAGUUAGUCCUU
GGACCUGAUCAGCUUGAAACAAGAACUACUGAUUCAACUUCUUUGGCUUAAUUCUC
GGAAACGAUGAAAUAUACAAGUUAUCUUGGUUUUCAGCUCUGCAUCGUUUGGGUUC
UCUUGGCUGUUACUGCAGGACCCAU AUGUACAAGAACGAGAAAACC
UUAAUGCAGGUCAUUCAGAUGUAGCGGAAUGGAACUCUUUCUUAGGCAUUUUGAAG
AAUUGGAAAGAGGGAGAGUGACAGAAAAAUAUGCAGGCCAAUUGUCUCCUUUACUU
CAAACUUUUAAAACUUAAAGAUGACCAGAGCAUCCAAAAGAGUGUGGAGACCAUCA
AGGAAGACAUGAAUGUCAAGUUUUCAAUAGCAACAAAAGAAACGAGAUGACUUCGAAA
AGCUGACUAAUAAUCGGUAACUGACUUGAAUGUCCAACGCAAAGCAAUACAUGAACUCA
UCCAAGUGAUGGCUGAACUGUCGCCAGCAGCUAAAACAGGGAGCGAAAAGGAGUCAG
AUGCUGUUUCGAGGUUGCAAGAGCAUCCAGUAAUGGUUGUCCUGCCUACAAUAAUUGAAU
UUUAAAUCUAAAUCUAAUUAUAAACAUUAAUAAUAGGAAUAAUAAUAGAC
UCAUCAAUCAAAGUAAUUAUAAUAGCAACUUUJUGUAAUAGAAAAGAAUAAUCUAAU
AAUAAUAGUAAUUAUUAUAAUCCUAAUCCUGUGACUGUCACUUAUCCUUUGUUU
CUGACUAAUAGGCAAGGCUAUGUGAUUACAAGGGCUUAUCUCAGGGGCCAACUAGGCA
GCCAACCUAAGCAAGAUCCCAUGGGUUGUGGUUAAUUCACUUGAUGAUACAAUGAAC
ACUUAUAAGUGAAGUGAUACUAUCCAGUUACUA

FIGURE 83A

Pneumocystis carinii (NUCLEOTIDES 84-415 OF ACCESSION # AF236872) (SEQ ID NO:331)

GAGGGUCAUGAAAGCGCGUGAAAACGUUAGCUAGUGAUCUGGAAUAAAUCAGAUUGC
GACACUGUCAAAJUGCGGGAAGCCC~~U~~AAAGAUCAACUACUAAGCAGUUUGUGGAAAC
ACAGCUGUGGCCGAGUUAAUAGCCCUGGGUAUAGUAACAAUGUUGAAU AUGAAUCUUUU
GCGAGAUGAAAUGGGUGAUCCGCAGCCAAGUCCUAAGGGCAUUUUUGUCUAUGGAUGCAG
UUCAACGACUAGAUGGCAGUGGGUAUUGUAAGGAAUUGCAGUUUCUUGCAGUGC~~U~~AA
GGUAUAGCUAUCCUCUUUCGAAAGAAAGAGUUAU

Candida albicans (NUCLEOTIDES 72-418 OF ACCESSION # X74272) (SEQ ID NO:332)

GGGAGGCAAAGUAGGGACGCCAUGGUUUCAGAAAUGGGCCGCGGUUUUUGACCUGC
UAGUCGAUCUGGCCAGACGUAUCUGUGGGUGGCCAGCGCGACAUACCUGGUACGGGG
AAGGCCUCGAAGCAGUGUUCACCUUGGGAGUGCGCAAGCACAAAGAGGUGAGUGGUGUA
UGGGUUAUCCCGUGGCGAGCCGUCAGGGCGCGAGUUCUGGCAGUGGCCGUCGUAGAG
CACGGAAAGGUUAUGGGCUGGCUCUCUGAGUCGGCUUAAGGUACGUGCCGUCCCACACGA
UGAAAAGUGUGCGGUGCAGAAUAGUUCACAGAACGAAGCUGCGCCGGAGAAAGCGAUU
UCUUGGAGCAAU

FIGURE 83B

Earwig R2 element (SEQ ID NO:333)

UAGGAUGAUAGCGCACCUGGUCAUCGUCUCUCUCAGCUGCUCACUUGCUGUUUCUAAGUG
AUAAUACCGUUGGUUUUUUAGUGGGUAUUCUUUUACGUUUCGUAGGGAGCGAGUCCCAC
ACUCUUGGAGCAAUCCGGGUAGUGCCUAAACGCAUUUCUCAACGU

Bombyx mori R2 element (SEQ ID NO:334)

GCCUUGCACAGUAGUCCAGCGGUAGGGUGUAGAUCAGGCCGUCUGUUUCUCCCCCGGA
GCUCGUCCCUUGGUUCCUUAAUAAUUUUAAACAUCAGAAACAGACAUAAACAUCUA
CUGAUCCAAUUUCGCCGGCGUACGGCCACGAUCGGGAGGGUGGGAAAUCUCGGGGUCUU
CCGAUCCUAAUCCAUGAUGAUUACGACCUGAGUCACUAAAGACGAUGGCAUGAUGAUCC
GGCGAUG